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        July 26, 2004, 21:20:15; Search time 6482 Seconds (without alignments) 10939.402 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have

REFERENCE AUTHORS

1 (bases 1 to 1636) Bridges, I.G., Grierson, D.

TITLE

Anti-sense

regulation

of plant gene expression

and

Schuch, W.W.

LOCUS
DEFINITION
ACCESSION
VERSION

L.esculentum polygalacturonase c A24194 A24194.1 GI:904404

Clone pTOM6.

linear

PAT

04-APR-1995

KEYWORDS SOURCE ORGANISM

Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

RESULT A24194

ALIGNMENTS

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result 1613.1 613.1 529.2 549.5 Score 1621 1621 1636 Query Match BB I01809 CPA505750 LES505947 AF152758 A24194 AR364905 A15981 AF152753 AF152755 AF152754 AY142668 PCCCHRAF AF152752 LEPG5 AF138858 AX651722 AX653992 BRA428543 MAUP14A A57101 AX016328 BNA250919 AF062467 RIAJ4147 BNPGALACR BNSAC66 AK117942 TOMPGAAA AY043233 AX062336 IJ AX654086 AX653993 TOMPGA AB084461 A62402 AY078936 PAPOLYGU AVOPOLYGAL LEPOLYGA LEPGR LEPG2AR 109042 L47242 Capsicum an AF152752 Actinidia AF152753 Actinidia AF152755 Actinidia AF152755 Actinidia AF152754 Actinidia AY142668 Arabidops A57101 Sequence 5 AX016328 Sequence Z49971 B.napus mRN A62402 Sequence 1 AJ428543 Brassica L27743 Malus domes AJ224147 Rubus ida AB084461 Pyrus com M20269 L.esculentu M37304 Tomato poly X14074 Tomato gene AK117942 Arabidops AX412563 Sequence AX651724 Sequence BT005576 Arabidops AX651722 Sequence AX653992 Sequence AX653993 Sequence I09042 Sequence 5 X66426 P.americana AY078936 Arabidops AJ250919 Brassica AF062467 Cucumis m I01809 Sequence 1 AJ505750 Carica pa AJ505947 Lycopersi AF152758 Actinidia AY043233 Vitis vin AX062336 Sequence X04583 Tomato mRNA X05656 Tomato mRNA I01809 Sequence 1 AJ505750 Carica pa X07410 Lycopersico AF138858 Lycopersi AX654086 Sequence Description A15981 L.esculentu AR364905 A24194 L.esculentu Sequence

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IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED
                             GTTCTTGCAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCT
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GTTCTTGCAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCT
                                                                                              AAAATTTAGTTGTTGGAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCAA
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/protein id="CAA01720.1"
/db_xref="GOA:PO5117"
/db_xref="GWISS-PROT:P05117"
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/mol_type="unassigned DNA"
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RESULT 2
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/AR364905 1636 bp Sequence 2 from patent US 5447867.

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03-SEP-2003

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AUTHORS
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1 (bases 1 to 1636)

Bridges, I., Schuch, W. and Grierson, D. Recombinant DNA containing pectin est Patent: US 5447867-A 2 05-SEP-1995; Location/Qualifiers
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Spermatophyta; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                    ATATTGACAAGGTTGATAAAAATGGGATTAAAGTGATTAATGTACTTAGCTTTGGAGCTA
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/protein_id="CAA01256.1"
/db_xref="GI:490040"
/db_xref="GOA:P05117"
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/clone="pTOM 6"
/tissue_type="fruit"
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                                                        CACTAGAAATTTCAGAGGATGAAGCTCTTTGTATAATTATTAATTTATACTATAGATCT
                                                                                                               AGGCTACGTGCAAAAATGTCCATTTTAACAATGCTGAACATGTTACACCACACTGCACTT
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Db 1501 THATMITHATHICHAITHTATHICHAITHTATHICHAITT	Db 1441 TCAATATATAGCAGATATGATATATCACAATAAACAAATCTATGTATTGTATTGAATAA 1500  Oy 1501 TTATTATTAATATGTACGGATTGAAGTTTTAATAAGAACTACTATGTATTTCTATTTCTA 1560
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REFERENCE
AUTHORS
TITLE
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ACCESSION
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Data kindly reviewed (22-APR-1987) by D. Grierson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 1621)

Grierson,D., Tucker,G.A., Keen,J., Ray,J., Bird,C.R. and Schuch,W.

Sequencing and identification of a cDNA clone for tomato
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Nucleic Acids Res.
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/db_xref="GGA:P05117"
/db_xref="SWISS-PROT:P05117"
/translation="MVUQRNSILLLIIIFASSISTCRSNVIDDNLFKQYYDNILEQEF
/translation="MVUQRNSILLLIIIFASSISTCRSNVIDDNLFKQYYDNILEQEF
AHDFOAYLSYLISKNIESNNNIDKYDKIRGIKVINVLSFGAKGDGKTYDNIAFEQAMNEA
CSSRTPVQFVVENNYLLKQIIFSGECRSSISVKIFGSLEASSKISDYKDRRLMIAF
CSSRTPVQFVVENNYLLKQIIFSGECRSSISVKIFGSLEASSKISDTIIGTGDDCISIV
PAVQALIVVGGGGTINMASAKSBUTDGHVSSUNYQYIQTSDTIIGTGDDCISIV
SGSQNVQATNITCGPGHGISIGSIGSGNSGAYVSNVTYNEAKIIGARSKYRTKTYGG
SGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATK
VAIKEDCSTNFPCEGIIMENINLVGESGKFSEATCKNVHFNNAEHVTPHCTSLEISED
                                                                                                                                      /product="mature 51. .263
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768. .776
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615. .623
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/db_xref="GI:19292"
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                                                                      CTATTATTGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAAAAIGTGCAGG
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1621
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 Biochim.
91316147
1859845
                                                                                               Tycopersicon esculentum (tomato)

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 1617)

Sheehy, R. E., Pearson, J., Brady, C. J. and Hiatt, W.R.

Molecular characterization of tomato fruit polygalacturonase

Mol. Gen. Genet. 208, 30-36 (1987)
                               Rogers,H.J., Allen,R.L., Hamilton,W.D. and Pollen specific cDNA clones from Zea mays Biochim. Biophys. Acta 1089 (3), 411-413
                                                                                                                                                                                                                                                                                        Tomato mRNA for polygalacturonase \mathbf{X05656}
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                                                                                                                                                                                                                                                       polygalacturonase
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Hiatt, W.R., Sheehy, R.E., Shewmaker, Pg gene and its use in plants
Patent: US 4801540-A 1 31-JAN-1989;
Calgene, Inc.; Davis, CA
Location/Qualifiers
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Submitted (13-AUG-2002)
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Isolation, cloning and characterization of polygalacturonase from ripening papaya fruit (Carica papaya cv. Singapore PP-1)
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                                                 AAATTTGATGATCAATGCTTCAGCAAAGAGCCCAAATACTGATGGAGTCCATGTATCAAA
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    TACTCAATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTTCAAT
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/codon_start=2
/codon_start=2
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GPTALTFWNCKNLKVNNLKSKNAQQIHLKFESCTNVJASNLMINASAKSPNTDGVHVSN
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/mol_type="mRNA"
/cultivar="Singapore PP-1"
/db_xref="taxon:3649"
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Saiprasad, G.V.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pg gene; polygalacturonase.
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolation, Cloning and characterization of polygalacturonase gene from fruit tissue of Lycopersicum esculentum cv. Arka vikas
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AJ505947.1 GI:34481842
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               GCTTTGGATT----GCTTTTGATAGTGTTCAAAATTTAGTTGTTGGAGGAGGAGGAAGTAT
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 AGAAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTACAAAGATAGAAG
                                                                     AGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAG
                                                                                                        ANACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATTTC
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GSLEASKISDYKDRELDCLLKSVQNLVVEGGGTINGMGQVMMPSSCKINKSLPCRD
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                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="pg"
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Direct Submission
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                                                                                                                                                            /mol_type="mRNA"
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                                                                                                       'gene="PGA"
                                                                                                                     tissue_type="fruit pericarp"
                                                                                                                                                 clone="CkPGA-3"
                                                                                                                                                                                       organism="Actinidia
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Submitted (19-MAY-1999) Plant Development, HortResearch, Bag 92169, Auckland, New Zealand
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/codon_start=1
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/db_xref="q01:7959983"
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FKAYPSYITTIGDNDFGSSMSHENGIFGLRKVDYGMDRVLDASKTVNVDDFGAKGDGS
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                                                                                                                GTGGTGAATGGAGCTAAGCTTTGTGGAACTACAAATGGAGTCAGGATTAAGACATGGCAG
                        TATCCCATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGTATACAACAGTTT
                                                                                 GGAGGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAG
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                                                                                                                                                                                              CATGGTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTT
                                                                                                                                                                                                                                                                                                                           GTATCAAATACTCAATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGT
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                                                                                                                                                                                                                                                                                                                                                                                      GTAGCTTCAAATTTGATGATCAATGCTTCAGCAAAGAGCCCCAAATACTGATGGAGTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCTAAAGAGTAAAAATGCACAAACAAATTCATATCAAATTTTGAGTCATGCACTAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGGGAGACACTGGCTTGTATTTGATAGTGTTCAAAATCTAAGGGTTGAAGGAGGTGGA
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                                                      GGGGGATCTGGAAGTGCAAGCAACATCAAATTTCAGAATGTGGAAATGCATAATGTGGAA
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Pred. No. 1.9e-76;
0; Mismatches 328;
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Query Match Best Local S Matches 815

tch 32.1%; al Similarity 65.6%; 815; Conservative

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Score 525.2; DB Pred. No. 1e-72; O; Mismatches 4

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Adelaide, Waite Campus, Glen (
3 (bases 1 to 1595)
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Vitis vinifera
AY043233
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Fincher, G.B.
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Nunan, K.J., Davies, C.,
Expression patterns of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGGCTGTCCAAGTGAAAAATATTTTCTACAAGAACATCAAAGGCACATGTGCCTCCAAT
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GSGSASNIKFQNIVMHNVENPIIIDQKYCDQSKPCKSQSSAVQVQNVLYQNIKGTSSS
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                                                                                                                                                                                                                                                                       /organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Shiraz"
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                                                                                           ACATTGATATAAAAGTTGGAGGAGGAAAGGCAGCCAAAGCTGTATGCAGCAATGCCAGAG 1351
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Plant Mol. Biol. 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 7456)
Bird,C.R., Smith,C.J., Ray,J.A., Moureau,P., Bevan,M.W.,
Hughes,S., Morris,P.C., Grierson,D. and Schuch,W.
The tomato polygalacturonase gene and ripening-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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SGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATK
VAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHCTSLEISED
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mol_type="genomic_DNA"
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al Similarity
462; Conserv
                                                                                                        Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 7456)
Bird,C.R., Smith,C.J., Ray,J.A., Moureau,P., Bevan,M.W., Bird,A.S.,
Hughes,S., Morris,P.C., Grierson,D. and Schuch,W.
The tomato polygalacturonase gene and ripening-specific expression
                                                                                                                                                                                                                                                                                                              Tomato gene for cel
X14074
X14074.1 GI:19305
                                                                                                                                                                                                                                                                                            polygalacturonase.
                                          in transgenic plants
Plant Mol. Biol. 11, 651-662 (1988)
Plant Mol. Biol. 11, 651-662 (1988)
Location/Qualifiers
1. 7456
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="polygalacturonase
6788. .>7048
/note="polygalacturonase"
/number=9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5711. .6138
/note="polygalacturonase
6139. .6255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="polygalacturonase intron F (no splice consensus);
putative"
5602. .5710
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number=7
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Pred. No. 5.3e-63;
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CAAT_signal
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1161 CAGTITTCAGCAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCA
                                                          tch 28.2%; So al Similarity 100.0%; J 462; Conservative 0;
                                                                                                                                                                                                                                                                    /number=7
6139. .625
                                                                                                                                                                                                                                                                                                            5602. .5710
/number=7
5711. .6138
                                                                                                                                                                                                                                  /number=8
6256. .678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SMISS-PROT: D05117"
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CSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKLFGSLEASSKISDYKDRRLWIAF
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GQQASNIKFLNVEMQDVKYPIIIDQNYCDRVEDCIQOFSAVQVKNVVYENIKGTSATK
VAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHCTSLEISED
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7244
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/db xref="taxon:4081"
/clone_lib="lambda EMBL.
877. .904
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6788. .7244
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4260. .44
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3717 .4259
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/db_xref="GI:295813"
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4260. .4467,4567. .4648,5602. .5710,6139. .6255,6788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  number=5
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                                                          Score 462; DB 8; ]; Pred. No. 5.3e-63; 0; Mismatches 0;
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                                                                                              Length 7456;
                                                              Indels
                                                            0;
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KEYWORDS SOURCE ORGANISM

REFERENCE

FEATURES

Gaps

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JOURNAL TITLE DEFINITION ACCESSION VERSION

RESULT 13 LEPOLYGA

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AK117942
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                                                                            source
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AKI17942.1 GI:26450945

FII CDNA; CAP trapper:
Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                              Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Scienc Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:msekigsc.riken.go.jp, URL:http://pfgweb.gsc.riken.go.jp, Tel:81-45-503-9625, Fax:81-45-503-9586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Only in Database (2002)

2 (bases 1 to 1600)

Seki, M., Tida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Saki, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Nakajina, M., Enju, A., Kamiya, A., Narusaka, K., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK117942 1600 bp mRNA linear PLN 06-Arabidopsis thaliana At3g57510 mRNA for putative endo-polygalacturonase, complete cds, clone: RAFL19-13-H11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Kawai, J., Hayashizaki, Y. and Shinozaki, K. Arabidopsis thaliana full-length cDNA
                                                                                                                                                   Please visit our web site (http://pfgweb.gsc.riken.go.jp/)
                                                                                                                                                                           This clone is in a modified pBluescript vector.
                                                                                                                                                                                                                                                                                                         An Arabidopsis full-length cDNA library was constructed essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTTTTTAATGTACAAAAATAATAAAAATGGTTATTTATATGA 1622
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                                                                                                                                                                                                reported previously (Seki et al. (1998) Plant J. 15:707-720; ki et al. (2002) Science 296:141-145). CDNA cleaved with BamHI d XhoI was ligated to modified Lambda FLC-1-E vector (Carninci (2001) Genomics 77:79-90) digested with BamHI and SalI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTITITATIGTACAAAATAATAAAATGGTTATTTATATGA 7246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGCTCTTTTGTATAATTATTAATTTATACTATAGATCTTCAATATATAGCAGATATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGTTTTCAGCAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCA 6844
/organism="Arabidopsis
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/cultivar="Columbia"
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P.,
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                          GTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTACTG
                                                                                                                                                                                                                                             CARATACTCAATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTTGAAAGTGAATAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAGATCCTAGGCACTTTATCAGCATCTACGAAACGTTCAGATTACAAAGACAAAAACC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTACAAAGATAGAAGGC 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAGTGTTTCAAACTTCGGAGCCAAAGGAGATGGAAAAACTGATGATACTCAGGCCTTCA
  GGATCAGCATTGGGGAGCTTGGGGGGACGACAATTCGAAAGCTTATGTCTCGGGAATTAATG
                                                                                                      CCATTGAGGATGGAACGCAAAATCTTCAAATCTTTGATTTAACTTGCGGCCCCCGGTCACG
                                                                                                                                           CAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATG
                                                                                                                                                                                                          CTAATACTCAAAACATTCGAGTCTCCAACTCAGATATCGGAACAGGTGATGATTGTATAT
                                                                                                                                                                                                                                                                                                               TTAGTAATGTTGAGATCACTGCTCCGGGCGATAGTCCCAACACAGATGGTATCCATATCA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAAGAGTAAAAATGCACAACAAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAAGCATGGAAGAAAGCATGTTCAACAAATGGAGTTACTACTTTCTTGGTTCCTAAAG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAATTTTGTGGTTCCTAAAA 396
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                                                                                                                                                                                                                                                                                                                                                                                                             TGAGGGTGAAAAATGCGCAGCAGATTCAGATTTCAATTGAGAAATGCAACAAAGTTGAAG
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ELVPKCKTYLLKSTRERGPCKGLRNFQLIGILSASTKESDTYDEXCHHLILTEDVNNLS;
DGGSTGIINGNCKTWWQNSCKIDKSKFCTKAFTALTLYNLKNLNVKNLRVKNAQQIQI
SIEKCMKVEVSNVEITAFGSSFNTDGIHITNYQNIKVSNSDIGTGDDCISIEDGTQNL
QIFDLTCGFGHGISIGSLGDDNSKAYVGSINVDGAFKSESDNGVRIKTYQGGSGTAKN
IKFQNIRMENVKNPIIDGDYCDKDKCEDQESAVQVKNVVYKNISGTSATDVAITLNC
SEKYPCQGIVLENVKIKGGTASCKNANVKNQGTVSFKCS"
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/protein_id="BAC42580.1"
/db_xref="GI:26450946"
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/codon_start=1
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/chromosome="3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1600
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Pred. No. 7.7e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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630

601 570 361

781 750 721 690 661

Query Match 27.2%; Score 445.2; DB 6; Length 1296; Best Local Similarity 64.7%; Pred. No. 3.4e-60; Matches 720; Conservative 0; Mismatches 368; Indels 24; Gaps 3;	/organism="Arabidopsis thaliana" /mol_type="unassigned_DNA" /db_xref="taxon:3702"	Syngenta Participations AG (CH); UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL (US); Glazebrook, Jan (US); Wang, Xun (US); Dangl, Jeffrey L. (US); Eulgem, Thomas (US)  FEATURES  Location/Qualifiers  source  11296	Plant genes, the expression of which are altered infection Patent: WO 0222675-A 327 21-MAR-2002;	a; Magnoliophyta; eudicotyledons; core sids II; Brassicales; Brassicaceae; Ara	KEYWORDS SOURCE Arabidopsis thaliana (thale cress) ORGANISM Arabidopsis thaliana Eukaryota: Viridinlantae: Strentonhuta: Embryonhuta: Typohoghuta	LOCUS AX412563 1296 bp DNA linear PAT 14-JUN-2002 DEFINITION Sequence 327 from Patent WO0222675. ACCESSION AX412563 VERSION AX412563.1 GI:21445021	RESULT 15 AX412563	H +	1 16	1 TAAACAAATCTATATCTATGTATGAATAATAATATTATTATTATATATA	QY 1411 TGTATAATTAATTAATTATAGATCTATAGATCTCAATATATAGCAGATATGATATATCACAA 1470	QY 1351 ATGCTGAACATGTTACACCACACTGCACTTCACTAGAAATTTCAGAGGATGAAGCTCTTT 1410	QY 1291 ATTTAGTAGGGGAAAGTGGAAAACCATCAGAGGCTACGTGGAAAAATGTCCATTTTAACA 1350	OY 1231 CCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATATAA 1290	Qy       1171 CAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCAACAAAGGTGG 1230	QY 1111 CCATAATTATAGACCAAAACTATTGTGATCGAGGTTGAACCATGTATACAACAGGTTTTCAG 1170	OY 1051 GATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAGTATC 1110	Qy 991 TAAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGAG 1050 
Qy 1291 ATTTAGTAGGGGAAAGTGGAAAACCATCAGAGGGTACGTGCAAAAATGTCCATTTTAACA 1350	Qy 1231 CCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATATAA 1290	1171 CAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCAACAAAGGTGG		OY 1051 GATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAAATGCAAGACGTTAAGTATC 1110	Qy 991 TAAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGAG 1050	Qy 931 GTATAAGTATTGGAAGCTTAGGAAATTCAGAAGCTTATGTGTCTAATGTTACTG 990	QY 871 CAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATG 930	743 CTAATACTCAAAACATTCGAGTCTCCAACTCAGATATCGGAACAGGTGATGATTGTATAT	Db 683 TEAGTAATGTTGAGATCACTGCTCCGGGCGATAGTCCCAACACAGATGGTATCCAATATCA 742  Qy 811 CAAATACTCAATATTTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTT 870		QY 691 TAAAGAGTAAAAATGCACAACAAATTCATATCAAATTTGAGTCACTAATGTTGTAG 750	Qy 631 GCAGGATCCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTGAAAGTGAATAATC 690	Qy 571 TCAATGGCAATGGACAAGTATGGTGGCCAAGTTCTTGCAAAATAAAT	2y 517 TTTGGATTGCTTTTGATAGTGTTCAAAATTTTAGTTGTTGGAGGAGGAGGAACTA 570	Qy 457 TAAAGATTTTTGGATCCTTAGAAGGCATCTAGTAAAATTTCAGACTACAAAGATAGAAGGC 516	397 323	Qy 337 AGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAATTTGTGGTTCCTAAAA 396	Qy 277 TTAATGTACTTAGCTTTGGAGCTAAGGGTGATGGAAAACATATGATAATATTGCATTTG 336

Db 1265 ATCAAGGCACCGTTTCTCCTAAATGCTCTAA 1296
Search completed: July 27, 2004, 01:30:44
Job time: 6486 secs

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Result
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Sequence 457 AA;	This polygalacturonase (PG) is encoded by plasmid clone pTOM6 which is used to produce antisense mRNA (with an inverted sequence to that of PG mRNA) which is Inserted into a vector used to transform plants which thereafter have altered ripening properties. The inverted sequence and the PG mRNA form a doubte-stranged structure which inhibits ex- pression of the PG mRNA. See also AAN80488. (Updated on 25-MAR-2003 to correct PA field.)	Disclosure; Page ?; 22pp; English.	Recombinant DNA comprising promoter and terminator sequences - useful in plants for altering ripening properties esp. in tomatoes.	WPI; 1988-169271/25. N-PSDB; AAN80487.	Bridges IG, Schuch WW, Grierson D;	(ICIL ) IMPERIAL CHEM IND PLC. (ZENE ) ZENECA LTD.	11-NOV-1986; 86GB-00026879.	06-NOV-1987; 87EP-00309853.	22-JUN-1988.	EP271988-A.	Unidentified.	Fruit ripening; polygalacturonase; pectin esterase.	Polygalacturonase.	25-MAR-2003 (revised) 20-NOV-1990 (first entry)	AAP80299;	RESULT 1 AAP80299 ID AAP80299 standard; protein; 457 AA.	ALIGNMENTS	29.6 422	709.5 29.7 515 5 ABB90945 Abb90945	715 29.9 392 5 ABB92116	718 30.0 435 5 ABB93472 Abb93472	724.5 30.3 398 5 AAE20568 Ade20568	741.5 31.0 491 5 ABB90812 Abb90812	764 32.0 453 4 AAM51693 Aam51693 Aam51691 Aam51691	767 32.1 460 2 AAR69791 Aar69791 Japoni	787 32.9 514 2 AAY25666 Aay25666 787 32.9 514 7 ADC34914 AdC34914	787 32.9 514 2 AAR93599 Aar93599	787 32.9 514 2 AAR53690 Aar53690	787.5 32.9 514 7	787.5 32.9 514 2 AAR81586 Aar81586 Cedar	

Query Match
Best Local Similarity

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Score 2390; DB 1; Pred. No. 7.3e-194;

Length 457;

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  cDNA of gene may act as a probe of modulating the production of
                                                                      Disclosure; Page; Bpp; English.
                                                                                                                         Tomato polygalacturonase gene - ucells or directing expression of
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17-OCT-1986;
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RESULT 3
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Best Local Similarity 100.0%;
Matches 457; Conservative
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25-MAR-2003
05-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 457 AA;
                                                                                                                                                                         polygalacturonase; PG; pectin esterase; PE; expression regulation; fruit softening enzymes; flowering plants; fruiting plants; antisense RNA.
                                                                                                                                                                                                                                                                                                          AAR32/107 standard;
                                                                                                                                                                                                                     Polygalacturonase.
                                                                                    06-NOV-1987;
                                                                                                          17-MAR-1993
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         Bridges IG,
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Pred. No. 7.3e-194;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA for flowering and fruiting plants e.g. tomatoes ripening control - comprises base sequence for transcription contg. inverted sequence of bases complementary to bases in anti sense ribonucleic acid encoding softening enzymes, or gene expression regulation.
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                                         in; pectin methylesterase; PME; polygalacturonase; PG; tomato; pTON
product; yogurt; milk; fruit juice; whey drink; de-esterification.
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                                                                                         polygalacturonase (PG)
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Matches 457
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                                                                   YCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNEPCEGIIMENINLVGESG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVIQRNSILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIE
KPSEATCKNVHFNNAEHVTPHCTSLEISEDEALLYNY
                                                                                                          GSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQN
                                                                                                                                                                            ASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSL
                                                                                                                                                                                                                                              WWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMIN
                                                                                                                                                                                                                                                                                                                  LKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2390; DB 4;
100.0%; Pred. No. 7.3e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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KPSEATCKNVHFNNAEHVTPHCTSLEISEDEALLYNY

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                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 452
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to forming an ester or amide bond between monomeric or polymeric ester or its acid or salt and monomeric or polymeric alcohol or amine by treating the ester or its acid or salt with a plant pectin transester synthase in the presence of alcohol or amine under conditions to form ester or amide bond. The method is useful for forming an ester or amide bond between monomeric or polymeric ester or its acid or salt (e.g. homogalacturonan) and monomeric or polymeric alcohol or amine. It is useful for producing pectin-based polymers e.g., xyloglucan or D- or L-polylysine, useful for the slow release of compounds in the body e.g., heparin with anticoagulant or other pharmaceutical properties. The present sequence represents an endopolygalacturonase enzyme from tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Formation of ester or amide bond between ester and alcohol involves treating the ester or its acid or salt with plant transester synthase in the presence of alcohol or amine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-2001; 2001US-0316777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant; pectin transester synthase; xyloglucan; polylysine; heparin;
anticoagulant; endopolygalacturonase; enzyme; tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR43936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albersheim P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomato endopolygalacturonase
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                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                    121
                            241
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                                                                                                                                                                                                                                                                                                         al Similarity
452; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      456
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                                                                                                                                           LKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQV
                                                                                                                                                                                    SNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYL
                                                                                                                                                                                                      SNNNIDKYDKYGIKVINYLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYL
                                                                                                                                                                                                                                                            MVIQRNSILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIE
                            ASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSL
                                                                              WWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMIN
                                                                                                                                                                                                                                              MVIQRNSILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIE
 ASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSL
                                                            WWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMIN
                                                                                                                        LKQITFSVDKNSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 18; 67pp; English.
                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                      97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456
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                                                                                                                                                                                                                                                                                                         Score 2338.5; DB 6
Pred. No. 1.7e-189;
0; Mismatches 4;
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                                                                                                                                 Matches
                                                                                                                                            Query Match
Best Local 8
                                                                                                                                                                                                                     for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value greater by a factor of 3 than the B-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidal; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicidally active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                  The invention relates to identifying target proteins (ABB90790-ABB94016)
                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                     organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tietjen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-2001; 2001WO-EP009892
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                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                           5; SEQ ID NO 1454; 261pp + Sequence Listing; English
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                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                 NNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLL 121
                                                                                                                                                                                     438
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                                                                             KQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVW 181
                                                                                                      ILLLIIIFASSISTCRSNV---IDDNLFKQ----VYDNILEQEFAHDFQAYLSYLSKNIES
                           KNRHGYAPRSSPRSFNVNTFGAKANGND-DSKAFMKAWEAACSSTGIVYIVAPKNRDYML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weidler
                                                                                                                                 Conservative
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                                                                                                                                            49.6%;
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                                                                                                                                 Score 1185; DB 5;
Pred. No. 1.2e-91;
6; Mismatches 121
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RESULT 7
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KW ESJZ
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seed production. The promoter is used to drive expression of a further nucleic acid sequence that results in prevention or reduction of anther dehiscence. For example, expression of the RNase barnase causes cell ablation, while expression of a plant hormone alters the developmental fate of a cell. Plants are produced that have phenotypically normal pollen grains, within phenotypically normal anthers, but in which the anthers do not dehisce and thus do not release the pollen grains. The system allows the female to be multiplied with the artificial male sterility gene in the homozygous state, since the female plant produces viable pollen. The system is suited to crops which have high seed multiplication, large amounts of pollen, and/or separate male and female inflorescences. These factors allow for easy collection of pollen from
                                                                                                                                                                                                                                                                                                                                                       thaliana. The invention relates to the use of the ESJ2A promoter to reduce dehiscence and to create male sterile plants for use in hybri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESJ2A gene;
transgenic J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation of male sterile plants by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-254279/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anther-specific ESJ2A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOG-)
                                                                                                                                                                                                                                                                                                                                                                                                                protein is encoded by the ESJ2A gene (see AAX25011)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 3; 34pp; English.
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Best Local
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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                                                                                                                                                                                                                                           EP1033405-A2
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                                                                                                                                                                                                                                                                                                                                                 sequence.
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99US-0123180P.
99US-0123548P.
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49.6%;
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                                                                          KIKG-
                                                                                            NLVGESGKPSEATCKNVHFNNAEHVTPHCT
                                                                                                                                    PIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENI
                                                                                                                                                           GISIGSLGDDNSKAYVSGINVDGAKFSESDNGVRIKTYQGGSGTAKNIKFQNIRMENVKN
                                                                                                                                                                          GISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKY
                                                                                                                                                                                                   VŚNVETTAPGDŚPŃTDGIHITŃTQNIRVŚNSDIGTGDDCIŚIEDGTQNLQIFDLTCGPGH
                                                                                                                                                                                                                   ASNLMINASAKSPNTDGVHVSNTQVIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGH
                                                                                                                                                                                                                                                                INGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
                                                                                                                                                                                                                                                                                         GKTYLLKSTRFRGPCKSLRNFQILGTLSASTKRSDYKDKNHWLILEDVNNLSIDGGSTGI
                                                                                                                                                                                                                                                                                                     NKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GT
                                                                                                                                                                                                                                                                                                                                   ETTLEAS-----TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLVPK
                                                                                                                                                                                                                                                                                                                                                    SKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPK
                                                                                                                                                                                                                                                                                                                                                                                                SILLLIIIFASSISTCRSNVID------DNLFKQVYDNILEQEFAHDFQAYLSYL
                                                                                                                 PIIIDQDYCDK-DKCEDQESAVQVKNVVYKNISGTSATDVAITLNCSEKYPCQGIVLENV
                                                                                                                                                                                                                                               INGNGKTWWQNSCKIDKSKPCTKAPTALTLYNLKNLNVKNLRVKNAQQIQISIEKCNKVE
                                                                                                                                                                                                                                                                                                                                                                              AVFLCVLLMLSLCKALSSNVDDGYGHEDGSFESDSLLKLNNDDVL
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99US-0159331P.
                                                                        -GTASCKNANVKNOGTVSPKCS
                   protein;
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S-0159329P.
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9.4e-87;
nes 116;
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Matches 223;
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to access comprising array.....g for herbicidally active compounds, comprising array.....g for herbicidally active compounds, comprising array.....g for herbicidally active compounds, comprising array. In such actions a sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for the polypeptides or nucleic acids encoding them are useful as
                                                                                                                                                                                                                                                                                                                                                                         Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
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                GISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKY
                                                                           ASNIMINĀSĀKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGH
                                                                                                                              INGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
                                                                                                                                                                                    NKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GT
                                                                                                                                                                                                                                  SKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPK
                                                                                                                                                                                                                                                                                           SILLLIIIFASSISTCRSNVID-------DNLFKQVYDNILEQEFAHDFQAYLSYL
  GISIGSLGDDNSKAYVSGINVDGAKFSESDNGVRIKTYQGGSGTAKNIKFQNIRMENVKN
                                                    VŚNVE TRAPGDŚPNTDGIHITNTON IRVSNSDIGTGDDCISIEDGTONLOIFDLTCGPGH
                                                                                                        INGNGKTWWQNSCKIDKSKPCTKAPTALTLYNLKNLNVKNLRVKNAQQIQISIEKCNKVB
                                                                                                                                                                                                                ETTLEAS-
                                                                                                                                                                                                                                                                  AVFICVILMISICKALSSNVDDGYGHEDGSFESDSLLKLNNDDVL-----SLISSD
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                     Score 1127; DB 5;
Pred. No. 9.4e-87;
1; Mismatches 116;
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PIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENI

PIIIDQDYCDK-DKCEDQESAVQVKNVVYKNISGTSATDVAITLNCSEKYPCQGIVLENV

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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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S-0139459P.
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Best Local S
Matches 223
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                                                                                                   Local Sim hes 223;
                  95
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                                           SKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPK
                                                                                                      Conservative
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99US-0151303P
99US-01513303P
99US-015363P
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99US-015363P
99US-0154018P
99US-0155413P
99US-0155458
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99US-0155659
99US-0157117P
99US-0157158
99US-0158232P
99US-0158232P
99US-015923A
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99US-0159331P
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99US-0149922P.
99US-0149922P.
99US-0149930P.
99US-0150866P.
99US-0150884P.
99US-0151065P.
                                                                                           47.2%; 5
49.6%; Pred
71;
                                                                                                   Score 1127; DB 3;
Pred. No. 1e-86;
1; Mismatches 116;
                                                                                                                              Length
                                                                                                    Indels
                                                                                                                                 463;
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RESULT 11
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XX AAG41
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05-MAR-1999
09-MAR-1999
23-MAR-1999
23-MAR-1999
06-APR-1999
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16-APR-1999
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310-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIIIDQDYCDK-DKCEDQESAVQVKNVVYKNISGTSATDVAITLNCSEKYPCQGIVLENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIIIDQNYCDRVEBCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFDCEGIIMENI
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99US-0121825P
99US-0123180P
99US-0125788P
99US-012564P
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99US-0126785P
99US-0128234P
99US-0129845P
99US-0130610P
99US-0130510P
99US-0130510P
99US-0131449P
99US-0132048P
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expression control;
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promoter;
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0-JUL-1999; 0-JUL-1999; 1-JUL-1999; 1-JUL-1999; 1-JUL-1999; 2-JUL-1999; 2-JUL-1999; 2-JUL-1999; 2-JUL-1999; 2-JUL-1999; 3-JUL-1999; 3-JUL-1999;		14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 18-MAY-1999; 19-MAY-1999; 20-MAY-1999;
99US-0144352P 99US-0144632P 99US-0144884P 99US-0145086P 99US-0145085P 99US-0145085P 99US-0145087P 99US-0145087P 99US-0145192P 99US-0145192P 99US-0145192P 99US-0145192P 99US-0145145P 99US-0145218P	99US-0135629P 99US-0136392P 99US-0136782P 99US-0137528P 99US-0137528P 99US-0137528P 99US-013840P 99US-013840P 99US-013847P 99US-0139454P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139461P 99US-0139461P 99US-0139461P 99US-0139462P 99US-0139462P 99US-0139462P 99US-014085P 99US-014085P 99US-0144085P 99US-0144085P 99US-0144085P 99US-0144331P 99US-0144331P 99US-0144331P 99US-0144333P	99US-0134219P. 99US-0134370P. 99US-0134376BP. 99US-0134376BP. 99US-0134941P. 99US-0135124P.
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14-OCT-1999; 99US-01: 14-OCT-1999; 99US-01: 14-OCT-1999; 99US-01: 18-OCT-1999; 99US-01: 21-OCT-1999; 99US-01: 22-OCT-1999; 99US-01:	02-AUG-19 04-AUG-19 05-AUG-19 06-AUG-19 06-AUG-19 06-AUG-19 06-AUG-19 09-AUG-19 11-AUG-19 11-AUG-19 12-AUG-19 13-AUG-19 20-AUG-19 21-AUG-19 21-AUG-19 22-AUG-19 23-AUG-19 27-AUG-19 27-AUG	1999; 99US-01: 1999; 99US-01: 1999; 99US-01: 1999; 99US-01: 1999; 99US-01: 1999; 99US-01:

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RESULT 12
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28-OCT-1999;
28-OCT-1999;
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  Tietjen
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                                                                                       28-AUG-2001; 2001WO-EP009892
                                               (FARB ) BAYER
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hes 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFRGPCKSLRNFQILGTLSASTKRSDYKDKNHWLILEDVNNLSIDGGSTGIINGNGKTWW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTASCKNANVKNQGTVSPKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DK-DKCEDQESAVQVKNVVYKNISGTSATDVAITLNCSEKYPCQGIVLENVKIKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRVEPCIQOFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNSKAYVSGINVDGAKFSESDNGVRIKTYQGGSGTAKNIKFQNIRMENVKNPI
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                                                                                                                                                                                                                                                                           thaliana
                                                                                                                                                                                                                                                                                                                   plant;
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    Weidler
                                                                                                                                                                                                                                                                                                                                                                active
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99US-0161361P
99US-0161920P
99US-0161993P
99US-0162142P
                                                                                                                                                                                                                                                                                                                   agriculture;
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                                                                                                                                                                                                                                                                                                                                                              polypeptide
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Pred. No. 3.8e-86;
B; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415
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Best Local Sim
Matches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--
                                                                                                                                                                                                                                                                                                                                                             SLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIID
                                                                                                                                                                                                                                                                                                                                                                                                     VTAPADSPNTDGIHITNTQNIRVSESIIGTGDDCISIESGSQNVQINDITCGPGHGISIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETWWQNSCKRNKA-----KALTFYNSKSLIVKNLKVRNAQQIQISIEKCSNVQVSNVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSILLLIIIFASSISTCRSNVIDDNLFKQVY-----DNILEQEFAHDFQAYLSYLSKNIE
                                                                                                                                                                                                                                                                                  QDYCDK-SKCTTEKSAVQVKNVVYRDISGTSASENAITFNCSKNYPCQGIVLDRVNIKG-
                                                                                                                                                                                                                                                                                                            QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE
                                                                                                                                                                                                                                                                                                                                           SLGDDNSKAFVSGVTVDGAKLSGTDNGVRIKTYQGGSGTASNIIFQNIQMDNVKNPIIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLVTVFLLWALLMFSWCKASRISPNVYDHSYKRFKSDSLIKRR--EDITGLRSFVRASLR
                                                                                                                                                       standard; protein;
                                                                                                                                                                                                                                                        SGKPSEATCKNVHFNNAEHVTPHCTS
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Pred. No. 8.7e-86; 
4; Mismatches 117
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Polygalacturonase; seed pod; dehiscence; shatter;

cilseed

rape,

Oilseed 16-OCT-2003 14-DEC-1996 AAW04268;

rape

seed (revised) (first en

pod polygalacturonase

entry)

transgenic

plant;

antisense

plant;

DZ2

gene;

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Best Local Simi
Matches 221;
                AAY42649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A polygalacturonase (PG) (AAW04248) of oilseed rape cv. Rafal seed pods is useful for controlling dehiscence. Manipulation of the enzyme's activity can influence the timing of dehiscence. A cDNA clone (AAT33994) coding for the PG was isolated from a cDNA library of the rape seed pod dehiscence zone. PG nucleic acids (partic. antisense) can be used to regulate dehiscence in crop plants. (Updated on 16-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  S--
                standard;
                                                                                                                                                QNYCDK-DKCEQQESAVQVNNVVYRNIQGTSATDVAIMFNCSVKYPCQGIVLENVNIKG-
                                                                                                                                                                        QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE 418
                                                                                                                                                                                                         SLGDDNSKAYVSGINVDGATLSETDNGVRIKT
                                                                                                                                                                                                                                SLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIID
                                                                                                                                                                                                                                                                                     INASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIG
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                                                                                                                                                                                                                                                                                                                                              QVWWPSSCKINKSLPCRDAPTALIFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLM
                                                                                                                                                                                                                                                                                                                                                                                  KSIRFRGPCKSLRSFQILGTLSASTKRSDYSNDXNHWLILEDVNNLSIDGGSAGIVDGNG
                                                                                                                                                                                                                                                                                                                                                                                                             KQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGG--GTINGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLL
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                                                                                                                    SGKPSEATCKNVHFNNAEHVTPHC 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SILLLIIIFASSISTCRSNVID-----DNLFKQVYDNILEQEFAHDFQAYLSYLSKNIES
                                                                                                                                                                                                                                                                 ITAPGDSPNTDGIHIVATKNIRISNSDIGTGDDCISIEDGSQNVQINDLTCGPGHGISIG
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                                                                                       -GKASCKNVNVKDKGTVSPKC
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               protein;
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Pred. No. 1e-84;
0; Mismatches 125;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The presentence represents a B. napus Sac66 protein putative sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal transduction protein; dehiscence; male st shatter resistance; oilseed rape; Sac66 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 433
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                                                                                                                                                                                                                                                                           KQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGG--GTINGNG
      CNYCDK-DKCEQQESAVQVNNVVYRNIQGTSATDVAIMFNCSVKYPCQGIVLENVNIKG-
                                                                                                                                                                                                         QVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLM
                                                                                                                                                                                                                                                                                                                                   NNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLL
                                      QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE
                                                                                               SLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIID
                                                                                                                                                                                      KIWWQNSCKIDKSKPCTKAPTALTLYNLNNLNVKNLRVRNAQQIQISIEKCNSVDVKNVK
                                                                                                                                                                                                                                                 KSIRFRGPCKSLRSFQILGTLSASTKRSDYSNDKNHWLILEDVNNLSIDGGSAGIVDGNG
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                                                                                                                               ITAPGDSPNTDGIHIVATKNIRISNSDIGTGDDCISIEDGSQNVQINDLTCGPGHGISIG
                                                                                                                                                         INASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIG
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1103; DB Pred. No. 1e-84; Mismatches 1:
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                                                                                                                                                                                                                                                                                                                                                                                         During early ripening of peaches, tissue firmness decreases slowly and progressively. Towards the end of ripening, loss of tissue firmness is capid. This second stage of softening is called the "melting" stage. Crapid. This second stage of softening is called the "melting" stage. Cof softening. Ripe fruit remain relatively firm and maintain their shape throughout processing. Fruit of "melting" varieties show an increase in cathvity of endopolygalacturonase (EndopG) during ripening. Cof softening (PG) is believed to contribute to fruit softening through its action on intercellular and cell wall pectins. The sequence can be used to manipulate plants of the Rosaceae family, especially peach or prunus to either prevent or enhance capression of PG. The sequence can also be used in efficient breeding programmes. See also AAR48675, AAR48676. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                          Query Match
Best Local S
Matches 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ripening; melting; pectins; breeding; Prunus; Rosaceae; endopolygalacturonase; EndoPG; polygalacturonase; PG.
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25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding peach polygalacturonase (PG) and production of peach PG in rosaceae plants - for production of plants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-101199/12.
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 37-38; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-melting' phenotype.
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                                               RSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINK 190
                                                                                                                                                                                                                                                                                                                                            404 AA;
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  KSHLTMTIYGTIEASDDRSVYKDVTHWLIFDNVQSLLVVGPGWINGNGNRWWETHAK--B
                                                                                                              SSVKTISIANFGAKGNGAD-DTRAFEKAWKAACSSNGAIVLVVPQ-KTYLVRPIEFSGPC
                                                                                                                                                                       NGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPC
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                      NVHFNNAEHVTPHCT 443
                                             TRORSÁVOVKNÝLYONIRGTSÁSTDÁITFNCSOSVÝCOGÍVLONIOL---
                                                            IQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCK 428
                                                                                               SGVFVNGAKISGTSNGVRIKTWQGGSGSASNIVFQNVEMNDVTNPIIIDQNYCDHKNKDC
                                                                                                                 SNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCD-RVEPC 368
                                                                                                                                                GIHITNTKNITISSSVIGTGDDCISIVSGSQRVQATDITCGPGHGIRIGSLGEDNANDHV
                                                                                                                                                              GVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSIGSIGSGNSEAYV 309
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Search completed: July 21, 2004, 17:06:20 Job time: 99.9229 secs

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Database :
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1636
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS  RESULT 1  AA038415  AA038415  AA038415;  XX  ACC ACQ38415;  XX  Polygalacturonase; PG; pectin esterase; PE; expression regulation; FT CDS  FT CDS  FT CDS  FT CDS  FT CDS  FT CDS  ACC ACC ACC ACC ACC ACC ACC ACC ACC AC	24 236.6 14.5 1505 3 AAC50895 25 228 13.9 1410 2 AAQ66049 26 228 13.9 1479 2 AAQ66051 27 28 13.9 1479 2 AAQ66051 28 226.4 13.8 1545 2 AAQ66048 28 226.4 13.8 1395 2 AAQ66048 29 225.4 13.8 1395 2 AAQ66050 31 224.8 13.7 1733 2 AAT18102 32 224.8 13.7 1733 2 AAT18102 33 221.4 13.5 1236 7 AAQ84046 34 220.2 13.5 1236 7 AAQ84046 35 221 13.0 219 1 AAV71212 36 212 13.0 219 1 AAV71212 37 221 13.0 219 1 AAV71212 38 208.6 12.8 10.9 12.9 2 AAQ99159 20 21.0 175 10.8 1492 3 AAC32613 39 177.2 10.8 1492 3 AAC32613 40 175 10.7 442 6 ABL94109 41 151.8 10.5 1673 6 AAD32961 42 174.8 10.7 1496 2 AAQ66076 43 171.2 10.5 1673 6 AAD32961 44 151.8 9.3 1185 6 ABZ4715 AAC42340

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Query Match
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Matches 1636; Conserv
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CTATTATTGGAACAGGTGATGGTATTTCAATTGTTTCTGGATCTCAAAATGTGCAGG
                                                           AGAGCCCAAATACTGATGGAGTCCATGTATCAAATACTCAATATATTCAAATATCTGATA
                                           AGAGCCCAAATACTGATGGAGTCCATGTATCAAATACTCAATATATTCAAATATCTGATA
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CC The invention provides a new method for modifying pectin that involves CC providing a host having pectin methylesterase (PME) activity and CC polygalacturonase (PG) activity, transforming the host by silencing PG CC activity to provide an increased PME to PG ratio, preparing a PME extract CC from the transformed host, and using the PME extract to modify pectin. A CC an increased functionality to food products such as yogurt, milk/fruit CC in a pectin in a block-wise manner, and to de-esterify two or more CC adjacent galacturonic acid residue of a pectin on at least substantially CC sequence of pTOM6 encoding a PG enzyme. A nucleotide sequence (seq Id No. 3) encoding the PG enzyme which is deposited as pTOM23 with NCIMB CC (Accession number 12373) is also claimed. The sequence for seq ID No. 3
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                                                                                                                     Query Match
Best Local Similarity
Matches 1636; Conserv
                                                                                                                                                                                                                     This cDNA clone, encoding polygalacturonase (PG), is used to produce antisense mRNA (with an inverted sequence to that of PG mRNA) which is inserted into a vector used to transform plants which thereafter have altered ripening properties. The inverted sequence and the PG mRNA for double-stranded structure which inhibits expression of the PG mRNA. Se also AAN80488. (Updated on 25-MAR-2003 to correct PA field.)
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20-NOV-1990
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                                                                                                                                                                                         Sequence 1637 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression cassette, pFP-IRN1 useful for gene silencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS20853;
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An An an improved method for inhibiting the CC expression of a target gene in a cell, by expressing in the cell an CC expression cassette comprising a promoter operably linked to a sense or CC antisense targeting sequence having substantial identity to a subsequence CC of the target gene, and an inverted repeat (IR) of a subsequence of a NOS (nopaline synthase) gene, where the IR is unrelated to the targeting sequence. The expression cassette, pFP-IRN1 is constructed using a CC (5'-UTL) is derived from a plant heat shock 70 (hsp70) gene, the tomato CC (5'-UTL) is derived from a plant heat shock 70 (hsp70) gene, the tomato CC (polygalacturonase (PG) gene and an IR of the terminator of the Expression of endogenous genes and transgence, e.g. to regulating expression of endogenous genes and transgence, e.g. to regulate CC expression of endogenous plant phenotypes such as disease resistance, eflavour, protein or nutritional characteristics. The improved gene construct is used in functional genomics to determine the silencing construct is used in functional genomics to determine the throughput studies. Multiple transgence, and is suitable for high-transgene. The method is simple and rapid, and is suitable for high-transgence the limitial silencing trigger mediated through the inverted repeat region will apply to all of the transcripts. The present sequence represents the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reducing the expression of a target gene in a cell, comprises expressing in the cell an expression cassette comprising a promoter operably linked to a sense or antisense targeting sequence and an inverted repeat of a
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07-AUG-2001;
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2001US-00924197
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Sequence 5822 BP; 1689 A; 1275 C; 1292 G; 1566 T; 0 U; 0 Other;

Length 5822;

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pathogenic infecti bacterial, fungal g at least infection fungal or one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant t to

Claim 6; ij NO 557; 899pp; English

comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present securior a plant to illustrate the invention.

Sequence 1296 BP; 424 A; 244 C; 293 G; 335 Ή. 0 ų; 0 Other;

Query Match Best Local

Similarity

27.2%;

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Length 1296;

Ş В 8 귱 Ş 밁 Ś В Š B δ 밁 Š 밁 8 뮍 Ş В Ş Ş В В S Matches Local 720; 803 871 683 751 623 563 691 631 503 571 443 383 457 GTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTACTG CAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATG CCATTGAGGATGGAAAGCTAAATCTTCAAATCTTTGATTTAACTTGCGGCCCCCGGTCACG CTAATACTCAAAACATTCGAGTCTCCAACTCAGATATCGGAACAGGTGATGATTGTATAT CAAATACTCAATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTT TTAGTAATGTTGAGATCACTGCTCCGGGCGATAGTCCCAACACAGATGGTATCCATATCA CTTCAAATTTGATCAATCATCAGCAAAGAGCCCAAATACTGATGGAGTCCATGTAT TGAGGGTGAAAAATĞCGCAGCAGATTCAGATTTCAATTGAGAAATGCAACAAAGTTGAAG TAAAGAGTAAAAATGCACAACAAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAG GCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTGAAAATTAATC GCACAAAAGCTCCAACGCTCTTACTTTATACAATTTAAAGAATTTGAATGTGAAGAATC TTAATGGCAACGGAAAAACCTGGTGGCAGAACTCATGCAAAATCGACAAATCTAAGCCAT ATTGGCTTATCTTAGÀGGACGTTAACAATCTÀTCAATCGACGGTGGCTCGACGGGAATTA TTTGGATTGCTTTTGATAGTGTTCAAAATTTAGTTGTTGGAGGAGGA------GGAACTA TTCAGATCCTAGGCACTTTATCAGCATCTACGAAACGTTCAGATTACAAAGACAAAAAACC TAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAGGC GAAAGACTTATCTCCTTAAGTCTACTCGATTTAGAGGCCCATGCAAATCCTTACGTAACT ACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAG AGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAATTTTGTGGTTCCTAAAA 396 AGAAAGCATGGAAGAAGCATGTTCAACAAATGGAGTTACTACTTTCTTGGTTCCTAAAG TTAATGTACTTAGCTTTGGAGCTAAGGGTGATGGAAAAACATATGATAATATTGCATTTG TTAGTGTTTCAAACTTCGGAGCCAAAGGAGATGGAAAAACTGATGATACTCAGGCCTTCA Conservative 0; Score 445.2; DB 7 Pred. No. 6.5e-69; 0; Mismatches 368 368; Indels 24; 862 802 870 810 930 742 682 750 622 690 336 562 630 502 570 442 382 456 322 516 262

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GATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAGTATC
                   TGGATGGTGCTAAGTTCTCTGAGAGTGACAATGGAGTTAGGATTAAGACTTATCAGGGAG
                                   TAPATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGCCAGGGAG
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A cDNA clone (AAT33994), designated SAC66, codes for a polygalacturonase (AAW04248) that is expressed specifically in the dehiscence zone (DZ) of oilseed rape cv. Rafal seed pods. Degenerate PCR primers based on multiple sequence alignments of fruit- and pollen-specific polygalacturonases were used to amplify cDNA from the DZ. A PCR fragment (AAT33999) was generated and used to screen a DZ CDNA library, yielding clone SAC66. The gene can be used in transgenic crop plants to regulate pod dehiscence. Antisense sequences reduce or prevent dehiscence and hence loss of seed prior to harvesting. (Updated on 16-OCT-2003 to
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14-DEC-1996
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                                                                                                                                                                                                                                       Control of seed pod dehiscence - using polygalacturonase or sequences derived from polygalacturonase gene.
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                                                                                                                                                                                                                                                                                                                                                                                               (NICK-) NICKERSON BIOCHEM LTD
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TGGCCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATA
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Pred. No. 1.5e-64;
0; Mismatches 416;
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Transgenic plant containing dehiscence zone selective chimeric
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25-MAR-2003
08-JUL-1997
                   WPI; 1997-235901/21
                                       Ulvskov P,
                                                                        06-OCT-1995;
08-DEC-1995;
                                                                                                04-OCT-1996;
                                                          (PLBZ ) PLANT
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                                 Child R,
Petersen I
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                                                                                                                                                                                                                                                                                                                                              plant; antisense;
                                                                                                                                                                                                                                                                                                                                                     zone; endo-polygalacturonase;
                                                                                                                                                                                                                                                                                                                                                                    zone-selective endopolygalacturonase cDNA
                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(revised)
(first entry)
                                                        GENETIC SYSTEMS NV
                                                                        95EP-00402241.
95EP-00203328.
                                                                                               96WO-EP004313
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                                Van Onckelen H, P<sub>1</sub>
Bundgard Poulsen
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cDNA clone X (AAT63603) includes a coding sequence for oilseed rape dehiscence zone (DZ)-selective endopolygalacturonase (PG). DZ cDNA was subjected to PCR amplification using primers (see also AAT63605-08) based on conserved regions of PG amino acid sequences. PG-related clones (see also AAT63609-14) were identified, of which only Ipg35-8 was specific to the DZ. This clone was used to screen a DZ-selective cDNA library prepd. From poly-A+ RNA isolated from the DZ 6 wk after anthesis, yielding clone x. Ipg35-8 was also used to screen a genomic library to identify the DZ-utilised in novel chimeric genes to modify the dehiscence properties of transgenic plants, partic. the pod dehiscence properties of B. napus. This can improve the seed yield from the transformed plants. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified dehiscence properties, especially delayed pod dehiscence
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Query Match

Sequence 1631 BP; 554 A; 291 C; 339 G; 446 T;

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                                                    The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod c an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The prese sequence represents the DNA encoding a B. napus Sac66 protein
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P-PSDB; AAY42649.
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Sequence 1657 BP;

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                                                                                                                                                                                                                                                                               The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                    Seguence 1280
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Katagiri
                                                                                                                                                                                                                                                                         illustrate the invention.
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ADA70539 st. ADA70539; 20-NOV-2003

(first entry)

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Query Match
Best Local Similarity
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Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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31-JUL-1986
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29-APR-1988
29-APR-1988
29-APR-1988
21-MAY-1990
09-JUL-1990
09-JUL-1990
08-AUG-1991
               Producing transgenic plant of modified phenotype - is useful expression of heterologous genes which are light-inducible.
                                                                                           WPI; 1998-296772/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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      17-JAN-1985;
31-JUL-1986;
26-MAY-1987;
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26-OCT-1998
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86US-00891529.
87US-00054369.
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Pred. No. 4.7e-49;
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This is the nucleotide sequence of a tomato polygalacturonase genomic DNA Clone isolated from a genomic library by screening with polygalacturonase CDNA. The polygalacturonase gene promoter is active in at least the CC breaker through red fruit stage in tomato fruit, and can be used in a CC breaker through red fruit stage in tomato fruit, and can be used in a CC phenotype. In this method, regulatory regions from plant genes (and T-DNA CC and Ti or Ri plasmids) are manipulated for use with foreign sequences for introduction into plant cells to provide transformed plants having a CC phenotypic property that can be modulated. The invention is exemplified CC with light, seed and fruit specific promoters. Also claimed are methods CC with light, seed and fruit specific promoters. Also claimed are methods CC characteristic to fruit, modifying transcription in fruit tissue, modifying the phenotype of a plant to impart a desired characteristic to fruit, modifying transcription in fruit tissue, and CC expressing a heterologous DNA sequence of interest specifically in fruit CC plants which have historically not been Agrobacterium hosts. (Updated on CC 25-MAR-2003 to correct PR field.)
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Best Local Similarity
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25-JAN-1988;
15-MAR-1988;
29-APR-1988;
02-NOV-1988;
02-MAY-1990;
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14-SEP-1990
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                                                                                                                                 TTGCTCATGATTTTCAAGCTTATCTTTCTTATTTGAGCAAAAATATTGAAAGCAACAATA
                                                                                                                                                    TTGCTCATGATTTTCAAGCTTATCTTTCTTATTTGAGCAAAATATTGAAAGCAACAATA
                                                                                                                                                                                                 GCAATGTTATTGATGACAATTTATTCAAACAAGTTTATGATAATATTCTTGAACAAGAAT
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                                                                                                                                                                                                                                                                                                                               ANTCTTTTTCAATAGACAAGTTTAAAAAACCATACCATATAACAATATATCATGGTTATCC
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                               ATATTGACAAGGTTGATAAAAATGGGATTAAAGTGA
                                                                                        ATATTGACAAGGTTGATAAAAATGGGATTAAAGTGATTAATGTACTTAGCTTTGGAGCTA 300
                                                                                                                                                                                                                                                                  <u>AAAGGAATAGTATTCTCCTTCTCATTATTATTTTTGCTTCATCAATTTCAACTTGTAGAA</u>
AGGGTGATGGAAAAACATATGATAATATTGTAAGTATTTÄÄATÄTTGGAATATATTTGT 1788
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88US-00168190.
88US-00188361.
88US-00267685.
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90US-00550804.
90US-00582241.
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Pred. No. 4.
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APPLICATION NUMBER: US/08/24,866
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 720,629
FILING DATE: 25-JUN-1991
APPLICATION NUMBER: 419,779
FILING DATE: 29-SEP-1989
APPLICATION NUMBER: 119,614
FILING DATE: 12-NOV-1987
ID NO:2:
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Matches
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APPLICANT: COUPE, Simon Allan
APPLICANT: COUPE, Simon Allan
APPLICANT: JENKINS, Elizabeth Sarah
APPLICANT: JENKINS, ENZAbeth SARAH
TITLE OF INVENTION: CONTROL OF POD DEHISCENCE
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/941,532
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00757
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9506684.1
FILING DATE: 31-MAR-1995
                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 371-260
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                           NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1657 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                      FEATURE:
                                                                                                                                                                                      TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                               Score 420.4; DB 3;
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RESULT 3
US-09-051-239A-1
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Sequence No. 6420628
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APPLICANT: BUNDGARD POULGEN, Gert
APPLICANT: BUTDGARD POULGEN,
TITLE OF INVENTION: Seed Shattering
FILE REFERENCE: 2121-0138P
CURRENT APPLICATION NUMBER: US/09/051,239A
CURRENT FILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: PCT/EP96/04313
PRIOR APPLICATION NUMBER: PCT/EP96/04313
PRIOR FILING DATE: 1996-10-04
PRIOR FILING DATE: 1995-10-06
PRIOR PPLICATION NUMBER: EP 95 402241.4
PRIOR FILING DATE: 1995-10-06
PRIOR APPLICATION NUMBER: EP 95 203328.0
PRIOR PILING DATE: 1995-12-08
NUMBER: OF SEQ ID NOS: 14
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rength: 1631
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OTHER INFORMATION: 0
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ILOCATION: (95)...(1393)
OTHER INFORMATION: Location 821-837 = region of endo-PG
OTHER INFORMATION: corresponding to oligonucleotide PG1.
OTHER INFORMATION: Strain cv. Topaz.
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TYPE: DNA
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NAME/KEY: unsure
LOCATION: (1439)
OTHER INFORMATION: n =
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                           TAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTAC----AAAGATAGAA
                                                                         GAAAGACTTATCTCCTTAAGTCTATTAGATTCAGAGGCCCATGCAAATCTTTACGTAGCT
                                                                                                     ACAAGAATTATCTCCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAG
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TCCAGATCCTAGGCACTTTATCAGCTTCTACAAAACGATCGGATTACAGTAATGACAAGA
                                                                                                                                                 AGAAAGCATGGAAGAAGGCATGTTCAACAAATGGAGTTACTACTTTCTTAATTCCTAAAG
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BORKHARDT, Ber
SANDER, Lilli
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VAN ONCKELIN, Henri
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                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location 95-163 = region encoding the presumed endo-PG signal peptide.

Location 884-900 = region of the endo-PG cDNA corresponding to oligonucleotide PG3

Location 1059-1073 = region of the endo-PG cDNA complementary to oligonucleotide PG2

Location 1229-1245 = region of the endo-PG cDNA complementary to oligonucleotide PG5
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Pred. No. 3.1e-87;
0; Mismatches 383;
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                                                                                                                                                                                        RESULT 4
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                                                 Sequence 139, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
                   APPLICANT:
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Kuo, Mei-Chang;
Yeung, Siu-mei H.;
                                    Garman,
                                      Richard D;
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 1410 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
PILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Evers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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                                                                                                                                                                                                                                                                                                                                                               TCATCTAGAACACCTGTTCAATTTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAA 419
                            GGCCAATGTAAATGGGTCAATGGACGAGAAATTTGCAACGATCGTGATAGACCAACAGCC
                                                               AGTTCTTGCAAAATAAATAAATCACTGCCA-----TGCAGGGATGCACCAACGGCC
                                                                                                   ACAGGTTTTACTCTAATGGGTAAAGGTGTAATTGATGGGCAAGGAAAACAATGGTGGGCT
                                                                                                                                      CAAAATTTAGTTGTTGGAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCA 599
                                                                                                                                                                            GCGTACCAAAATCCAGCGAGCTGGAAGAATAATAGAATATGGTTGCAGTTTGCTAAACTT
                                                                                                                                                                                                               GCATCTAGTAAAATTTCAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTT
                                                                                                                                                                                                                                                                                ATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAGTAAAGATTTTTTGGATCCTTAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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RESULT 5
US-08-467-023-141
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Patent No. 6090386
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic Pharmaceutical Corporation,
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                               COUNTRY: U
ZIP: 02154
                                                                                                                                                 STREET:
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Bond, Julian F.;
Garman, Richard D;
                                                                                                                                                                                                                                                                                                       Kuo, Mei-Chang;
Yeung, Siu-mei H.;
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Best Local Similarity 52.3%;
Matches 557; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/35
FILING DATE: December 6,
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08, FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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AATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATGGTATAAGTATTGGAAGCTTA 950
                                                                ATATOTGATACTATTATTGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAA 890
                                                                                                                        GCTTCAGCAAAGAGCCCAAATACTGATGGAGTCCATGTATCAAATACTCAAATATATTCAA
                                  TTACAAAAGAACACGATAGGAACAGGGGATGACTGCGTCGCTATAGGCACAGGGTCTTCT
                                                                                                    GCACCGAGAGACAGTCCTAACÁCTGATGGAATTGÁTATCTTTGCATCTAÁAAÁCTTTCÁC
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REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 ТСАТСТАGAACACCTGTTCAATTTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAA
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                                                    CAAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAATTTGATGATCAAT
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GAATTTCATTTAGTTTTTGGGAATTGTGAGGGAGTAAAAATCATCGGCATTAGTATTACG
                                                                                                           ATTAAATTCGATTTTTCCACGGGTCTGATAATCCAAGGACTGAAACTAATGAACAGTCCC
                                                                                                                                                                                                                                                                                                                                      ACAGGTTTTACTCTAATGGGTAAAGGTGTAATTGATGGGCAAAGGAAAACAATGGTGGGCT
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Pred. No. 3.4e-43;
0; Mismatches 495
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US-08-467-023-133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
               TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC POOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
                                                       REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                 FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         APPLICATION NUMBER: US/08, FILING DATE: June 6, 1995 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 610 L. CITY: Waltham
                                                                                                       NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
                                                                                                                                                                                         APPLICATION NUMBER: 08/350,225
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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610 Lincoln St
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Exley, Mark A.;
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Yeung, Siu-mei H.;
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Bond, Julian F.;
Garman, Richard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Griffeth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrew;
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                                                                                               025.6 USD2
                                                                                                                                                                                                                                                                                                               Version
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Best Local Similarity
Matches 557; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE:
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TYPE: n
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LOCATION:
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                                       ATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAGTATCCCCATAATTATAGACCAAAAAC 1130
                                                                                                                   GGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAAC
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       ATAATTTATGAGAATGTTGAAATGATAAATTCGGAGAACCCCATATTAATAAATCAATTC
                                                                                   GACACACAAAATGGATTAAGAATCAAAACATGGCAGGGTGGTTCAGGCATGGCAAGCCAT
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52.3%;
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Pred. No. 3.6e-43;
0; Mismatches 495;
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US-08-467-023-140
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6090386
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/350,221
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-740
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                       TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pairs
TYPE: nucleic acid
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TITLE OF INVENTION: Allergenic Proteins And
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
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   TCATGATGCTATCAACATCTTCAATGTGGAAAAAGTATGGCGCAGTAGGCGATGGAAAGCA
                                TAAAAATGGGATTAAAGTGATTAATGTACTTAGCTTTGGAGCTAAGGGTGATGGAAAAAC
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Exley, Mark A.;
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Yeung, Siu-mei H.;
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Bond, Julian F.;
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                                                                                                                                                                      GGGCACAAGTGCAACAAAGGTGGCCATAAAATTTGATTGCAGCACAAACTTTCCATGTGA 1267
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Best Local Similarity
Matches 212; Conserva
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APPLICATION NUMBER: 06/920,574
FILING DATE: 17-OCT-86
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/845,676
FILING DATE: 28-MAR-86
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: DONNA E. Scherer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: KRIDL, J.
APPLICANT: HIATT, W.
APPLICANT: KNAUF, V.
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PRIOR APPLICATION DATA:
07/750,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: (916) 753-6313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/240,408 FILING DATE: 30-AUG-88
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CITY: Davis
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REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                       ATAATATTGCATTTGAGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAAT
TTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCA
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                                                                                                                                                                                                                   ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Schwedler
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                                                                                                                                                                                                                                                                                                                                             double
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                                                                                                                                                                                                                   13.0%; Score 212; DB 1; 100.0%; Pred. No. 8.4e-40; ive 0; Mismatches 0;
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                                                                                                                                                                                                                     Gaps
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IN PLANT/CELLS

NUMBER OF SEQUENCES: 2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/750,505

FILING DATE: 27-AUG-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 240,408

FILING DATE: 30-AUG-1988

FILING DATE: 30-AUG-1988
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5453566-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHEWMAKER, CHRISTINE K.; KRIDL, JEAN C.; HIATT, WILLIAM R.; KNAUF, VIC TITLE OF INVENTION: ANTISENSE REGULATION OF GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-941-532-7
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Best Local Similarity
Matches 212; Conserva
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ROBERTS, Jeremy Alan
APPLICANT: COUPE, Simon Allan
APPLICANT: JENKINS, Elizabeth Sarah
APPLICANT: JENKINS, Elizabeth Sarah
TITLE OF INVENTION: CONTROL OF POD DEHISCENCE
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,532
FILING DATE: 30-SEP-1997
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 920,574
FILING DATE: 17-OCT-1986
APPLICATION NUMBER: 845,676
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                                                                                                                                                       ZIP:
                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                              D.C.
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; Pred. No. 8.4e-40;
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RESULT 11
US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463 Patent No. 5670367
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/GB
FILING DATE: 29-WAR-1996
FRIOR APPLICATION DATA:
APPLICATION UMBER: GB 950
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                             STREET: 1800 Dia
CITY: Alexandria
 APPLICATION NUMBER:
                 FILING DATE:
                                                                                                                                                                                                                 COUNTRY:
                                                                                        APPLICATION NUMBER:
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TYPE: nucleic acid
STRANDENESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 GATTIAACTIGCGGCCCGGTCACGGCCTAGGT 162
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                                                                                                                                                                                                                                                           E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                   USA
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EP 91 114 300.6
                             US/07/935,313
                                                                                          US/08/232,463
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Pred. No. 5.6e-08;
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US-08-232-463-14
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 harr
Type-
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
1092 RRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCT 1053
                             1290 AATTTAGTAGGGGAAAGTGGAAAACCATCAGAGGCTACGT 1329
                                                                                                                                                  1170 GCAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCAACAAAGGTG 1229
                                                                                                                                                                                      1272
                                                                                                                                                                                                            1110 CCCATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGTATACAACAGTTTTCA 1169
                                                                                                                                                                                                                                                                                                    1230 GCCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATATA
                                                                                                                       990 GTAAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGA 1049
                                                                                                                                                                                                                                                                                                                                                                                           930 GGTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTACT 989
                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity 5.0%;
                                                           nucleic acid
                                                                                                                                                                                 GGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAGTAT 1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.00045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7218;
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; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION;
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEM!
; APPLICANT: WATANABE, HIDEM!
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DIA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-790-988-1
                                                                                 SEQ ID NO
                                                                                                        SOFTWARE: PatentIn Ver. 2.1
ORGANISM: Buchnera sp.
                            TYPE:
                                                  ENGTH: 640681
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Patent No. 6583275

Patent No. 6583275

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 125;
                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2998: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1451 GCAGATATGATATATCACAATAAACAAATCTATATCTATGTATTGAATAATTATTATTAA 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1391 TTCAGAGGATGAAGCTCTTTTGTATAATTATTATTATATTATACTATAGATCTTCAATATATA 1450
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMÁTION:
NAME: ARINIEllo, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1631 AAAAA 1635
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                HYPOTHETICAL: NO ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                         TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAA 325389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATAAATATTTTATATTTTÄÄTÄÄÄÄÄÄÄÄÄÄÄÄTÄTTTATATAAATAAATACTGATATTTT
                                                                                                 STRANDEDNESS:
                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                      LENGTH: 1356 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 0.035;
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    NAME/KEY: misc feature;
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    LOCATION: (B) LOCATION 1...1356
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SEQUENCE DESCRIPTION: SEQ ID NO: 2998:
US-09-107-532A-2998
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                                                                                                                                                                                                                                                                                                                     APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYI
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-790-988-1/c
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                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                     Best Local Si
Matches 154;
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                              LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera
                                                             609613 AAAGTAGCAATTTCAATAATACGATGTACTTTAGGATTCAGTCCAGTCATTTCTAAATCT
                                                                                          1333 AAAATGTCCATTTTAACAATGCTGAACATGTTACACCACACTGCACTTCACTAGAAATTT
1393 CAGAGGATGAAGCTCTTTTGTATAATTATTATTTATACTATAGATCTTCAATATATAGC 1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 TGTATCTATGCTCAAAATGTAGAGAACATCTCTGTCACTGGTTTCGGTACATTAGATGGA 342
                                                                                                                                                                                                                                                                     640681
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                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCAGTCACCAAGTTGGACGATCAACCCGATTCTTTGCAGTAATGCAACGTTTGATAAC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACCAACGGCCTTAACCTTCTGGAATTGCCAAAATTTGAAAGTGAATAATCTAAAGAGT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGGATCTCAAAATGTGCAGG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTTCAATTGTT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAATGCACAACAAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAAT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTABATTG----ATGAGTTTCCATAACTGTCATCGAATTACTGTGAAAGATATTAAATTG 459
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                                                                                                                                     Conservative
                                                                                                                                                         3.2%;
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47.9%; Pred. No. 0.0061;
tive 0; Mismatches 19
                                                                                                                                     Score 52; DB 4; Length 640681; Pred. No. 0.059; 0; Mismatches 145; Indels 5
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: S013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: DE 10019071
FRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-04-06
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-19
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US-10-204-708-19/c
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SEQ ID NO 19
LENGTH: 6866
Type: No.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.2%;
Best Local Similarity 49.8%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/10204708 Patent No. 6677731
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: DE 10043826.1 PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             609318 AATA 609315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609553 ATCCAGATTAAATTTTTTTTATTGATTTTTCATATTTTTCATAATTATTAAATATTTTTT 609494
1610 GTTATTTATATGAAAAAAAAAAAA 1632
                                                                                                                                                                                                                             2346
                                                                                                                                                                                                                                                                                                2406 ACACTACTCTABACTCTABAAAACTTACTAATABACAABACGAACATAAAACTTATATTCT
                                                                                                                                                                                                                                                                                                                                    1513
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                                                                                                                                                                         GTATTGAATAATTATTAATATGTACGGATTGAAGTTTTAATAAGACTACTATGTATT 1549
                                                                                                                                     AATAAAAAACTTATÄTÄÄÄAAAATATATATTATTATATATCÄTTÄTATÄÄAACTÄTTATTÄT
                                                                                                                                                                                                                                                    ACTATAGATCTTCAATATATAGCAGATATGATATATCACAATAAACAAATCTATATCTAT 1489
                                                        TCTATTTTCTAGTCAAAAGTTTGACGATTGTACTTTTTAATGTACAAAAATAATAATAATG 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTACGGATTGAAGTTTTAATAAGACTACTATGTATTTTCTATTTTCTAGTCAAAAGTTTG 1572
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                                                                                                                                                                                                                                                                                                                                                                            Score 51.8; DB 4; Length 6866; Pred. No. 0.014; 0; Mismatches 132; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                     2227
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2166 TTATTATATACTAAAAAAAAAAA 2144

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Search completed: July 27, 2004, 04:23:19 Job time: 135 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Sequence 9185, Ap Sequence 9185, Ap	73025,	Sequence 31774, A	0170,	50404,	9731, A	83751		3 ;	Sequence 498. Ann	31 Apr	5922	7729 A		43683		1430	Sequence 2520. An	2520.	Semience 95670 A	9854	865	9445	e 92601	e 59408	29325.	116781	Sequence 3, Appli

## ALIGNMENTS

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GCITI	AGTAJ       AGTAJ	AAACI      AAACI	Score Pred. 0; Mi	on US/09924197 . 30018993A1 Paul Improved Methods Repeat Sequences 76-010810US NUMBER: US/09/924 2001-08-07 MBER: 60/225,508 000-08-15 : 3 er. 2.1
GGAT	VAGAT	AAGAA        AAGAA	re lo d. No Misma	ds of ces
TGCT	ITCTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTT 	TTAT	Score 1042.4; DB 1 Pred. No. 3.5e-192; 0; Mismatches 6;	f Gene
ETTG!	GGATO	CITIC	e e	
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GENERAL INFORMATION:
APPLICANT: ULVSKOV, Peter
APPLICANT: VILLD, Robin
APPLICANT: VAN ONCKELIN, H
APPLICANT: PRINSEN, E1S
APPLICANT: BORKHARDT, BEST
APPLICANT: SANDER, Lilli
                                                                                                                                            Sequence 1, Application US/10151668 Publication No. US20020184660A1
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  CHILD, Robin
VAN ONCKELIN, I
PRINSEN, Els
BORKHARDT, Berr
SANDER, Lilli
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TITLE OF INVENTION: Seed Shattering
FILE REFERENCE: 2121-0138P
CURRENT APPLICATION NUMBER: US/10/151,668
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/051,239
PRIOR FILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: PCT/EP96/04313
PRIOR FILING DATE: 1996-10-04
PRIOR PLICATION NUMBER: EP 95 402241.4
PRIOR APPLICATION NUMBER: EP 95 203328.0
PRIOR FILING DATE: 1995-12-08
PRIOR FILING DATE: 1995-12-08
NUMBER OF SEQ ID NOS: 14
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LENGTH: 1631
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APPLICANT:
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LOCATION: (1439)
OTHER INFORMATION: S
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEATURE: PEATURE: Location 95-163 = region encoding the presumed OTHER INFORMATION: endo-PG signal peptide.
OTHER INFORMATION: Location 884-900 = region of the endo-PG cDNA OTHER INFORMATION: corresponding to oligonucleotide PG3
OTHER INFORMATION: Location 1059-1073 = region of the endo-PG cDNA OTHER INFORMATION: complementary to oligonucleotide PG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (95)...(1393)
LOCATION: (95)...(1393)
OTHER INFORMATION: Location 1229-1245 = region of the endo-PG
OTHER INFORMATION: complementary to oligonucleotide PG5
OTHER INFORMATION: Location 821-837 = region of endo-PG cDNA
OTHER INFORMATION: corresponding to oligonucleotide PG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Brassica napus
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                                                                                                                                                                                 ACCACTGGCTTATTTTGGAAGACGTTAATAATCTATCAATCGATGGCGGCTCGGCGGGA
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BUNDGARD POULSEN,
                                                 CATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTGAAAAGTGAATA 687
                                                                                                TTGTTGATGGCAACGGAAATATCTGGTGGCAAAACTCATGCAAAATCGACAAATCTAAGC
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Pred. No. 1.4e-71;
0; Mismatches 383;
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RESULT 3
US-10-437-963-24608
US-10-437-963-24608, Application US/10437963
; Publication No. US20040123343A1
; GEMERAL INFORMATION:
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                APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbaruk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 24608
LENGTH: 1359
TYPE: DNA
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
ORGANISM: Oryza sativa
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Pred. No. 7.6e-63;
0; Mismatches 425;
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_29575C.1
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
FILE REFERENCE: 
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Pred. No. 1e-61;
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PRIOR APPLICATION NUMBER: US 08/812,665
PRIOR APPLICATION NUMBER: US 08/484,941
PRIOR PRILING DATE: 1997-03-07
PRIOR PRILING DATE: 1995-06-07
PRIOR PRILING DATE: 1995-06-07
PRIOR PRILING DATE: 1993-08-10
PRIOR APPLICATION NUMBER: US 07/526,123
PRIOR APPLICATION NUMBER: US 07/526,123
PRIOR APPLICATION NUMBER: US 07/526,685
PRIOR PILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: US 06/692,605
PRIOR APPLICATION NUMBER: US 06/692,605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: AND EXPRESSION OF HETERO
FILE REFERENCE: 16518.052
CURRENT APPLICATION NUMBER: US/09/782,130
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: US 09/232,861
PRIOR FILING DATE: 1999-01-15
                                                                                        PRIOR FILING DATE: 1985-01-17
PRIOR APPLICATION NUMBER: US 07/582,241
PRIOR FILING DATE: 1990-09-14
PRIOR APPLICATION NUMBER: US 07/188,361
PRIOR FILING DATE: 1988-04-29
PRIOR APPLICATION NUMBER: US 07/168,190
PRIOR APPLICATION NUMBER: US 07/168,190
PRIOR FILING DATE: 1988-03-15
PRIOR FILING DATE: 1988-03-15
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                                NUMBER
                                                                                                                                                                                                                                                          FILING DATE: 1985-01-17
APPLICATION NUMBER: US 07/582,241
FILING DATE: 1990-09-14
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                                                                    Prior Application data removed
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RESULT 6
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                                                                                                                              PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 618
LENGTH: 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 618, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
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SEQ ID NO 26
LENGTH: 2207
                                TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: N region
LOCATION: (8)..(8)
OTHER INFORMATION: n = {
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
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Best Local Similarity 95.3%;
Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
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                    FEATURE:
NAME/KEY: N_region
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FILING DATE: 2001-09-26
APPLICATION NUMBER: US 60/370,620
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Goff, Stephen A.
Katagiri, Fumiyaki
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Briggs, Steven P.
Cooper, Bret
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Pred. No. 2.4e-54;
0; Mismatches 17
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; NAME/KEY: N region
; LOCATION: (190)..(190)
; OTHER INFORMATION: n =
US-10-260-238-618
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Best Local Similarity
Matches 613; Conserv
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NAME/KEY: N_region
LOCATION: (49)..(49)
OTHER INFORMATION: n = a
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NAME/KEY: N_region
LOCATION: (102)...(102)
OTHER INFORMATION: n =
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OTHER INFORMATION: n =
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                         TTCATCGACACCGTGCACCTCTATGGCACCACCAATGGAGCTCGGATCAAGACATGGCAG
                                                                                                                     CATGGTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTT
                                                                                                                                                              GTGTCGATCGAGGATGGGACCCACGGTTTACACGTCACGAGACTGGTGTGTGGGCCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                         PATCTAAAGAGTAAAAATGCACAACAAATTCATATCAAATTTGAGTCATGCACTAATGTT
                                                         ACTGTAAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAG
                                                                                           CATGGGATTAGCATTGGGAGCTTAGGAGATGACAACTCCAGAGCTGAGGTGTCTGACATC
                                                                                                                                                                                             ATTTCAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGT
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Pred. No. 1.2e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LAR Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 607
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APPLICANT:
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Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
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Publication No. US20040034888A1
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                    APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Koreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 30261
LENGTH: 1308
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 24666
LENGTH: 1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andre
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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TTTCCATGTGAAGGAATTATAATGGAGAATATAAATTT 1294
                                                                                                                                                                                                                                                    ACGAATGGAGCTCGCATCAAGACATGGCAGGGAGGAAAGGGTTCAGCGAAGAACATCGTG
                                                                                                                                                                                                                                                                                   GAAAATGGAGTTAGGATCAAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAACTGCCCAAACACCGATGGCATCCACATCACACGCAGCAGAGATGTTCAGGTGACA
                                      AAGAACATCAGGGGCACAAGTGCATCAGAGGAGGCCATCGTGCTGCATTGCAGCAACAGT
                                                                                                         GACTCTTCTACACCCTGCAAGCAACAGAAATCTGCAGTGGAGGTGAGCAATTTGCTGTTC
                                                                                                                                          GATCGAGTTGAACCATGTATACAACAGTTTTCAGCAGTTCAAGTGAAAAATGTGGTGTAT 1196
                                                                                                                                                                                                         TTTCTGAATGTGGAAATGCAAGACGTTAAGTATCCCATAATTATAGACCAAAACTATTGT
                                                                                                                                                                                                                                                                                                                        CATAATTCTGAAGCTCATGTCAACAATGTCACCGTGGACAATGTCAGGCTGTATGGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGCCACAATATTACTTGTGGTCCAGGTCATGGTATAAGTATTGGAAGCTTAAGATCT
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                                                                        GAGAATATCAAGGGCACAAGTGCAACAAAGGTGGCCATAAAATTTGATTGCAGCACAAAC 1256
                                                                                                                                                                                                                                                                                                                                                                                              CATGTCAAGAACATGGTGTGGACCGGGACACGGCATCAGCATCGGCAGCTTGGGGGAT
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Pred. No. 1.3e-34;
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Sequence 61964, Application US/10424599

Publication No. US20040031072A1

GENERAL IMFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 61964
LENCTH: 1333
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ORGANISM: Glycine
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                                                                                                                      GGATACAGCAGTTCTTAGGGAGACTACCAACGGTCTCAGAATTAAGACTTGGCAGGGAGG
                                                                                                                                                                                  AATCAGCATTGGAAGTCTAGGGAAAGACAACTCAACAGGCATAGTCACGAAAGTGATTTT
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                            CATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGTATACAACAGTTTTCAGC
                                                                                        ATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATGCCAAGACGTTAAGTATCC
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CGGCTCGAGAGACCAATTTTACTGTGATTCTCCAACCAATTGTGAAAATCAGGCATCAGC
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APPLICANT: Zhou, Yīhua
APPLICANT: Zhou, Yīhua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 10970
LENGTH: 1219
TYPE: DNA
ORGANISM: Glycine max
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Publication No. US20040034888A1
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Best Local
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387; Conserv
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                                      TAGGATCAAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGT 1087
                                                                                                                                                                                   AATTTATTGTGGACCAGGACATGGAATCAGCATTGGAAGTCTAGGGAAAGACAACTCAAC
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                                                                                                                                                                                                                                                                                                                      TGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAA 907
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CAGAATTAAGACTTGGCAGGGAGGTTCTGGATATGTTCGAGGGGTGCGTTTTCAGAATGT
                                                                                        AGGCATAGTCACGAAAGTGATTTTGGATACAGCAGTTCTTAGGGAGACTACCAACGGTCT
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Pred. No. 1.7e-28;
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecul
TITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 141807
LENGTH: 1479
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 Matches 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_99063C.1
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CCCAATGGAAAAACTTTGTCAGGGCCATGTGGTAGTCCTGCTATGATACGGTTCTTCATG
                                                                                                      GATAGCCGCAATCAATGGCTTGTATTTTATCGACCTGACCAAATGACTCTTAATGGTACA
                                                  GGAACCATTGAAGGGAATGGAGACAAATGGTGGGATCTCCCCTGCAAGCCTCACAGGGGT
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                          TGCAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAAT
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Pred. No. 8e-28;
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GAACCATGTATACAACAGTTTTCAGCAGTTCAAGTGAAAAATGTGGTGTATGAGAATATC
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                                                        GA---ATGTCTAAACCAGACTTCAGCTGTGCATGTGAATGATGTCTCCTACAGCAACATA
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Sequence 874, Application Patent No. US20020023280A1 GENERAL INFORMATION: APPLICANT: Gorlach, Jorn PRIOR APPLICATION NUMBER: 60/178,502 PRIOR FILING DATE: 2000-01-27 NUMBER OF SEQ ID NOS: 999 APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences o:
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26 Kricker, maj Ledford, Brooke L. Woessner, Jeffrey P. Haas, William David Davis, Keith R. Allen, Keith Matthew, Abraham V. Ledford, Brooke L. An, Yong-Qiang Hamilton, Carol Price, Jennifer Garcia, Carlos A. Page, Amy Rameaka, Joshua Yu, Yang Tracy Maja US/09770444 Q гз of Arabidopsis

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LENGTH: 442
TYPE: DNA
CORGANISM: Arabidopsis
US-09-770-444-874
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                                                                                                                    US-09-924-035A-369
                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/148,784;
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SEQ ID NO 369
LENGTH: 442
TYPES
                                                                                                                                                                                                                                                                                                                             Sequence 369, Application US/09924035A Patent No. US20020142319A1 GENERAL INFORMATION:
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Best Local
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                                                            Matches
                                                                            Best Local Similarity
                                                                                       Query Match
                                                                                                                                                                                                                                           FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
                                                                                                                                                                                                                                                                                       APPLICANT: Grlach, Jrn
TITLE OF INVENTION: Expressed Sequences
TITLE OF INVENTION: thaliana
                                                                                                                                TYPE: DNA ORGANISM: Arabidopsis thaliana
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Local Similarity 65.0%;
les 275; Conservative
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                                 TCAGAAGCTTATGTGTCTAATGTTACTGTAAATGAAGCCAAAATTATCGGTGCCGAAAAT
       TCAGAAGCATATGTTTCAAATGTGGTAGTCAACAAAGCGACTCTTATAGGAACCACTAAT
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Publication No. US20040049809A1

GENERAL INFORMATION:
APPLICANT: Institute de Cincia Aplicada e Tecnologia (ICAT)
APPLICANTION: Pear genes codifying for b-Galactosidase, Pectin Methylesterase,
TITLE OF INVENTION: Polygalacturonase, Expansin and their use.
FILE REFERENCE: none
CURRENT APPLICATION NUMBER: US/10/362,091
CURRENT PILING DATE: 2003-02-12
PRIOR APPLICATION UMBER: PT 102511 C
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                    Matches 360;
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NAME/KEY: CDS
LOCATION: (112)...(1
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                 699 AAAAATGCACAAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAAT
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CAATATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTTCAATTGTT 878
                                                                                          TTGATGATGATGAGCTTCAGCAAAGAGCCCCAAATACTGATGGAGTCCATGTATCAAATACT
                                                                                                                                                   CTAAACAGCCAAATGTTCCACATTGTCGTCAACGGCTGCCAAAATGTGAAAATGCAAGGT
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Pred. No. 3.2e-23;
0; Mismatches 293;
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TCTGGAGTCACCATTCTCGACTCCAAAATTTCAACCGGTGACGACTGTGTCTCAGTTGGC

Search	Db	γQ	Db	VQ VQ	Φb	Ş	Db	Qy	Db	γQ	Дb	γQ	Db	γQ
Search completed. July 27 2004 04.26.07	1162 AAATTCGATTGTAGTTCCATGTATCCTTGCAACGGGATCAGACTGCAAGATGTGAA 1217	1236 AAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATATAAA 1291	1102 AAGGTCAGCGATGTGACGTATCAAGACATTCATGGTACATCGGCGACGGAAGTGGCGGTG 1161	1176 CAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCAAACAAA	1042 GTTATTGATCAAAATTACTGCCCTAATGACAAAGGTTGCCCTGGCCAAGCTTCTGGAGTT 1101	1116 ATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGTATACAACAGTTTTCAGCAGTT 1175	982 GGATTTGCTAGGAGCATTCTTTTCCAACATATTGTGATGACCAACGTTCAAAATCCAATC 1041	1056 GGACAAGCTAGCAACATCAAATTTTCTGAATGTGGAAATGCAAGAGGTTAAGTATCCCATA 1115	922 GTTACATTCACTGGTACTGAAAACGGCGTCAGAATTAAGTCTTGGGGGAGACCTAGCACT 981	999 GCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGAGGATCT 1055	862 ATTGGGAGTTTAGGGAAGGACCAACAAGAAGCCGGTGTACAAAATGTTACAGTTAAAACA 921	939 ATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTACTGTAAATGAA 998	802 CCCGGCACTACCAATTTGTGGAATTGAAAACGTCGCATGTGGACCCGGCCACGGAATCAGC 861	879 TCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATGGTATAAGT 938

Search completed: July 27, 2004, 04:36:07 Job time: 766 secs

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

BM413004 EST587331	BM413004	12	774	46.1	754	4
BM412528 EST586855	BM412528	12	767	46.8	765.4	. w
BM412817 EST587144	BM412817	12	786	47.1	770	2
BM410796 EST585123	12 BM410796	12	797	47.6	778.6	ין
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Description	ID	B	Match Length DB	Match	Score	No.
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5 742 45.4 742 12 BM413282 BM41 7 726.4 44.4 728 12 BM413343 BM41 7 726.4 44.4 728 12 BM413343 BM41 7 726.4 44.4 728 12 BM413375 AM42 8 709 43.3 729 10 AW422257 9 707.4 42.4 696 10 AW422253 AW44 1 683.8 41.2 703 12 BM408546 BM33 6 673.8 41.2 677 10 AW422353 AW44 4 670.2 41.0 675 12 BM408546 BM33 6 643.3 9.1 677 10 AW221785 AW42 9 642.4 39.3 644 10 AW423400 AW42200 9 642.4 39.1 639 10 AW221785 AW22 7 654.4 40.0 672 10 AW221785 AW22 9 642.4 39.3 644 10 AW423600 AW42 9 642.4 39.1 639 10 AW223600 AW22 9 642.4 39.1 639 10 BE434493 BE43493 BM33 1 623.1 38.4 632 10 BE43493 BM34 1 623.3 38.4 632 10 BE432845 BE43 1 623.3 38.4 632 10 BE433931 BE43 1 623.3 38.4 623 12 BM409552 BM41 1 623.4 36.9 604 10 BE430331 BE43 9 602.4 36.9 604 10 BE430331 BE43 9 602.4 36.9 604 10 BE431800 BE33 1 597.4 36.4 598 10 AW22391 1 597.4 35.7 593 10 AW22391 1 583.4 35.7 593 10 AW22391 1 583.4 35.7 593 10 AW22366 1 597.3 35.0 500 10 AW22366 1 597.4 35.7 593 10 AW22366 1 597.4 35.7 593 10 AW22366 1 597.4 35.7 593 10 AW22366 1 597.4 34.9 572 10 AW22366 1 597.4 34.9 5872 10 AW22366 2 595.4 34.9 5872 10 AW22366 3 567 34.9 588 10 BE43253 4 8022 595.4 563 10 BE43253 5 670.4 34.9 588 10 BE43253 5 670.4 34.9 588 10 BE33253 AW22 2 595.4 588 10 BE33253 AW22 3 567 34.9 588 10 BE33253 AW22 3 568 34.9 588 10 BE33253 AW22 3 56	ST41232	46091	6091	10	σ	4	•	5
5         742         45.4         742         12         BMM413282         BMM413332         ENT58767           7         726.4         44.4         728         12         BM413075         ENT58767           7         726.4         44.4         728         12         BM413075         ENT587767           7         709.4         43.2         709         10         AW422257         AW41939         BRT131133           9         707.4         43.2         696         10         AW42253         AW42233         AW42233         EST311134           1         694.4         41.2         696         10         AW42233         AW42233         EST311134           2         674.4         41.2         677         10         AW42233         EST311134           2         677.2         40.2         677         10         AW42233         EST311137           3         673.8         41.0         672         10         AW222222         EST31167           4         627.2         40.2         677         10         AW422340         AW221785         EST29893           5         643.3         33.3         643         10         AW22	ST31079	4140	4140	10	S.	4.	o.	14
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413392         BST58760           7         726.4         44.4         728         12         BM413075         BM413075         BM413075         BST587707           7         70.4         43.3         729         10         AW422257         AW422257         BM723257         BST5878103           8         70.7         4         43.2         696         10         AW442335         AW442335         BST311131           1         683.8         41.2         677         10         AW422335         BM53089         BST311131           2         6670.2         41.0         677         12         BM408546         BM7228222         BST739131           5         6570.2         40.2         672         10         AW221785         BM722990         BM442241         EST398287           6         657         40.2         672         10         AW221785         AW221785         BST729832           6         657         40.0         672         10         AW42280         BW410534         BW42280         BST731114           8 </td <td>ST40554</td> <td>3446</td> <td>3446</td> <td>10</td> <td>g</td> <td>4.</td> <td>σŊ.</td> <td>3</td>	ST40554	3446	3446	10	g	4.	σŊ.	3
742 45.4 742 12 BM413282 EM413282 EST58766 738 45.1 748 12 BM413343 EM413282 EST58766 726.4 44.4 728 12 BM413375 EM4131375 EST58767 727.4 43.3 729 10 AW421339 AW421257 EST29906 694.4 42.4 696 10 AW442253 694.4 42.4 696 10 AW442233 683.8 41.8 687 10 AW442233 673.8 41.2 677 10 AW442231 673.8 41.2 70.1 12 BM410846 657.2 40.2 677 12 BM410847 657.2 40.2 677 12 BM411547 BM412421 EST388287 657.4 40.0 675 12 BM410847 657.2 40.2 677 10 AW42221785 654.4 40.0 677 10 AW2221785 642.4 39.3 644 10 AW4223400 AW221785 EST29903 642.4 39.3 644 10 AW4223400 AW221785 EST29859 630.4 39.3 644 10 AW4223400 AW422340 EST391167 630.4 39.3 644 10 AW4223400 AW422340 EST391167 628.8 38.1 639 10 AW442280 AW422340 EST391167 628.4 38.4 632 10 BE432845 628.3 38.1 632 11 BE432845 628.3 38.1 632 11 BM413202 628.4 38.4 632 10 BE432845 628.3 38.1 632 11 BM413202 628.4 38.4 632 10 BE432845 628.3 38.1 632 11 BM413202 629.8 83.4 632 10 BE432845 629.8 38.4 632 10 BE432845 629.8 38.1 632 11 BM413202 629.8 38.1 632 11 BM413202 629.8 38.1 632 12 BM410252 617.4 37.7 61.1 10 BE432845 629.8 38.4 632 10 BE432845 629.8 38.4 632 10 BE432845 629.8 38.4 632 10 BE432845 629.8 38.4 639 10 AW222391 620.4 36.9 604 10 BE432831 620.3 36.9 604 10 BE432835 620.4 38.4 599 10 AW222391 620.4 36.4 599 10 AW222391 620.4 36.8 601 10 AW222391 620.4 36.9 604 10 BE433180 620.4 36.9 604 10 BE	ST30047	2366	2366	10	σ	.4	g	2
\$ 742 45.4 742 12 BM413282 BM413282 BST58766 738 45.4 749 12 BM413075 7726.4 44.4 728 12 BM413075 7726.4 44.4 728 12 BM413075 8 709 43.3 729 10 AW422257 8 709 43.3 709 10 AW422257 9 707.4 42.4 696 10 AW422253 2 674 41.2 679 10 AW42233 2 673.8 41.2 677 12 BM413039 4 6570.2 40.2 677 12 BM41547 6 657.2 40.2 677 12 BM412547 6 657.4 40.2 677 10 AW422272 6 654.4 40.0 6672 10 AW222272 7 654.4 40.0 6672 10 AW2221785 8 642.4 39.3 644 10 AW222183 9 642.4 39.3 644 10 AW422280 9 642.4 39.3 644 10 BE433493 9 662.0 38.4 632 10 BE434493 9 628.8 38.4 632 10 BE434493 9 628.8 38.4 632 10 BE4332845 9 660.3 38.1 623 12 BM410538 9 660.4 36.9 604 10 BE4332845 9 662.4 36.9 604 10 BE433180 9 663.4 604 10 BE433180 9 664.4 605 10 AW222835 9 66	ST39906	3253	3253	10	æ	4.	70.	1
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413283         BM4131343         BM4131343         BM4131343         BM4131343         BM4131343         BM4131343         BST58760           7         72.3         44.4         72.8         12         BM413075         BM4131343         BST58740           7         70.9         43.3         72.9         10         AW422257         BST311133           9         694.4         42.4         696         10         AW422335         AW442233         BM736689         BM442233         BST3311133           1         683.8         41.2         677         12         AW42224         BM436846         BST3818143           1         683.8         41.2         677         12         AW422241         AW42234         BM408546         BST331163           1         677         40.2         677         12         AW422241         BM408546         BST38183           4         470.2         677         12         AW422241         BM408546         BST331133           4         670.2         40.2         677         12         AW422183         BM41	ST29954	2273	2273	10	~	4.	70.	0
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413283         BM4131282         EST58760           7         726.4         44.4         728         12         BM413075         BM413075         BM413075         EST58740           7         726.4         44.4         728         12         BM413075         EST58740           7         726.4         42.4         696         10         AW422257         AW44233         EST311133           0         694.4         42.4         696         10         AW442333         AW442233         EST311173           1         683.8         41.2         677         10         AW442241         AW442234         EST31173           2         677.2         41.0         675         12         BM408546         BST311547           4         670.2         41.0         672         10         AW22242         AW42241         EST31173           3         673.4         40.0         672         10         AW22242         AW42241         EST3158911           4         670.2         40.2         677         10         AW422241         <	ST30027	2346	2346	10	~	5	-1	39
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413282         BM4131343         BM4131343         BM4131343         EST58767           7         726.4         44.4         728         12         BM413075         BM413075         BM413075         BM4113075         BM413282         BM413282         BM4113075         BM413282         BM412233         BM412233         BM412242 </td <td>ST29967</td> <td>2286</td> <td>2286</td> <td>10</td> <td>J</td> <td>5</td> <td>74.</td> <td>88</td>	ST29967	2286	2286	10	J	5	74.	88
5 742 45.4 742 12 BM413282 BM413282 BST58760 738 45.1 749 12 BM413075 BM413193 BST58760 778.4 44.4 728 12 BM413075 BM4131075 BST587670 70.7.4 43.2 70.9 10 AW442233 AW442233 AW442233 BST311133 AW442233 BST311133 AW442233 BST311133 BM442233 BST311133 BM442233 BST311133 BM442233 BST311133 BM442233 BST311133 BM442234 BM442233 BST311133 BM442234 BM44	ST58347	0914	0914	12	æ	5	57	37
5 742 45.4 742 12 BM413282 BM413282 BM413282 BST58760 73.8 45.4 74.9 12 BM413075 BM4131343 BM413143 BST58760 77.6 44.4 72.8 12 BM413075 BM4131343 BM413075 BM4131075 BM41311133 BM413139 BM31311313 BM413139 BM31311313 BM413139 BM31311313 BM413139 BM3131133 BM413139 BM3131133 BM413133 BM413235 BM3131133 BM413235 BM3131133 BM413235 BM3131133 BM413235 BM3131133 BM413235 BM3131133 BM413235 BM413235 BM3131133 BM413235 BM413235 BM3131133 BM413235 BM4132	ST31089	4149	4149	10	0	5	œ	86
5         742         45.4         742         12         BM413282         BM413282         BM41343         BM41343         BM41343         BM41343         BM41343         BM413143         BM413143         BM413143         BM413143         BM413143         BST58767           7         726.4         44.4         728         12         BM413075         BM413075         BM413075         BM413075         BM413075         BM413075         BM413075         BM411075         BM413075         AW442237         BM413075         BM4141039         BST311137         BM414141         AW442234         BM414223         BM442234         BM442234         BM442234         BM442234         BM442241         BM442241         BM442241         BM442242         BST58820         BM442	ST29953	2272	2272	10	9	<u>ب</u>	83.	5
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413282         BM413283         BM4131282         BM4131282         EST58760           7         726.4         44.4         728         12         BM413075         BM413075         BM413075         BM413075         BM4131075         AW422257         BST29906         AW442339         BM4142233         BST311133         AW442234         BM442233         BM442233         BST331163         AW442233         BM442234         BST358911         AW442234         BM442234         BM415360         BM442234         BM442234         BST35894         BM442234         BM442234         BST35894         BM442234         BM415360         BM442234         BST3	ST40803	3691	3691	10	œ	ū	83.	34
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413283         BM413283         BM413283         BM413283         BM413283         BM413283         BM413283         BM413275         BM412257         BM412257         BM412257         BM41239         BM41239         BM322257         BST29906         90707.4         43.2         709         10         AW422253         AW442233         BM442233         BST3311433         AW442234         BM441233         BST3311433         AW442234         BM442234         BM442234         BM442234         BM442234         BM442235         BM33608         BM442234         BM442244         BM442244 <td>ST31159</td> <td>4219</td> <td>4219</td> <td>10</td> <td>0</td> <td>5</td> <td>œ</td> <td>ü</td>	ST31159	4219	4219	10	0	5	œ	ü
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413283         BM413243         BM413243         BM413243         BM413243         BM413243         BM413243         BM413243         BM413275         BM4122257         BST587906         AW422257         BST229906         AW442253         AW442233         BM422257         BST311133         AW442233         AW442233         BM432253         BST331133         AW442233         BM3536089         BM536089         BM536089         BST588211         AW442233         BM4422241         BM536089         BST588211         AW442233         BM4422241         BM536089         BST588211         AW442241         BM536089         BST588211         AW442241         BM536089         BST581163         AW442241         BM536089         BST581163         AW442241         BM536089         BST588211         AW442241         BM536089         BST381163         BM443224         BST31163         BM442241         BM536089         BST58821         AW442241         BM411547         BM4122	ST30072	2391	2391	10	S	6	95.	32
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413282         BM413243         BM413243         BM413243         BM413243         BM413243         BM413243         BM413243         BM413275         BM4131075         BM413293         BM414233         BM414233         BM414233         BM414233         BM414233         BM442235         BM442233         BST3311133         BM442233         BM442233         BST3311133         BM442233         BM442233         BST3311133         BM442233         BM442233         BM442233         BM442233         BST3311133         BM442233         BM442233         BM442233         BM442233         BM442233         BM442233         BM442233         BM442233         BM442234         BM536089         BST3511133         BM442234         BM536089         BST3511133         BM442234         BM536089         BST3511133         BM442234         BM442234         BST3511133         BM442234         BM442234         BST351133         BM442234         BM442234         BST358911         BM442234         BM442234         BST358136	ST29964	2283	2283	10	0	9	97.	31
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413283         BM413283         BM413283         BM413283         BM413283         BM413275         BM412275         BM413275         BM422257         BST29906         PST287916         PST287916         PST287916         PST287916         PST287916         PST287916         PST28791173         PST2879173         PST28799173         PST28799173         PST28799173         PST28799173         PST28799173         PST28799173         PST28799173         PST28799173         PST28799173         PST298793         PST298793         PST298793         PST298793         PST298793         PST298793         PST29	ST41262	6120	6120	10	0	9	02.	30
5         742         45.4         742         12         BM413282         BM413282         BM41343         BM4144223         BM313113         BM4144223         BM313113         BM414223         BM313113         BM41343         BM41343         BM41343         BM413434         BM413434         BM413434         BM413434         BM413434         BM413434         BM413434         BM413434         BM413444234 <t< td=""><td>ST39970</td><td>3318</td><td>3318</td><td>10</td><td><math>\mathbf{L}</math></td><td>6</td><td>60</td><td>29</td></t<>	ST39970	3318	3318	10	$\mathbf{L}$	6	60	29
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413282         BM413283         BM413283         BM413283         BM413283         BM413283         BM413275         BM412257         BST258740         AW422257         BST29906         AW442335         AW442233         BM412257         BST311133         AW442233         BM442233         BST331133         AW442233         BST331133         AW442233         BST331133         AW442233         BST331133         AW442233         BST331133         AW442233         BM442233         BM443233         BST331133         AW442233         BM443233         BST331133         AW442233         BM443233         BM443234         BM536089         BST588911         AW442233         BM443233         BST331133         BM443233         BST331133         BM443234         BM443234         BST31133         BM443234         BST38891         BM443234         BST38891         BM443224         BST38891         BM442234 </td <td>ST39985</td> <td>3332</td> <td>3332</td> <td>10</td> <td>C</td> <td>9</td> <td>0</td> <td>28</td>	ST39985	3332	3332	10	C	9	0	28
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413343         BM41339         BM413343         BM41339         BM41339         BM3131133         AM422257         BM722257         BST29906         AW442233         BM441233         BM441233         BM336089         BM442234         BM442235         BST311173         BM442234         BM442235         BST311173         BM442234         BM442234         BM442234         BM442234         BM442234         BM442234         BM442234         BM442234         BM442244         BM442244         BM408546         BST358911         AW42234         BM408546         BST3589287         BM408546         BST358287         BM408546         BST3589287         BM408546         BM408546         BST358287         BM408546         BM408546         BST358287         BM408546         BM408546         BM41547         BM42221785         BM408546	ST41235	6093	6093	10	$\mathbf{L}$	7.	$\vdash$	27
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM41343         BM41347         BM41344	ST58752	1320	1320	12	$\mathbf{L}$	7.	17.	26
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM41343         BM41343         EST58760           7         726.4         44.4         728         12         BM413075         BM412075         AW442237         AW442237         AW442237         AW442237         AW442233         BM31133         BM31143         BM4142234         BM412234         BM41328         BM442233         BST331113         BM442233         BM442233         BM442233         BM442233         BM31343         BM442234         BM31343         BM314328         BM31343         BM31343         BM31343         BM31343         BM31343         BM314328         BM31343         BM314328         BM31343         BM31343         BM314328         BM31343         BM314328         BM3134328         BM3134323         BM3134328         BM31342233 <td>ST58357</td> <td>0925</td> <td>0925</td> <td>12</td> <td>V3</td> <td>ω.</td> <td>N</td> <td>25</td>	ST58357	0925	0925	12	V3	ω.	N	25
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413283         BM413295         BM413295         BM413283         BM413295         BM412257         BST258740         PST289906         PST289131133         PST311133         PST311133         PM442233         BM442233         BST3311133         PM442233         BM442233         BST3311133         PM442233         BM442233         BST3311133         PM442233         BM442233         BST3311133         PM442233         BM442233         BM442234         BST3311133         BM408546         BST331143         BM408546         BST38184         BM408546         BST38184         BM408546         BST38287         BM408546         BST38287         BM408546         BST38287         BM408546         BST	ST33642	3161	3161	10	w	8	28.	24
5         742         45.4         742         12         BM413282         BM413282         BM41343         BM41374         BM41374         BM41374         BM41374         BM41374         BM41343         BM41374         BM41274         BM41374         BM41274	ST39947	3284	3284	10	w	8	28.	23
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM41343         BM5758740           7         726.4         44.4         728         12         BM413075         BM413075         BM413075         BM413075         BM413075         BM5758740           7         726.4         43.3         729         10         AW422257         AW422257         BST29906           8         709         43.2         709         10         AW442339         AW442253         BST331133           9         694.4         42.4         696         10         AW442253         AW442233         EST331133           1         683.8         41.8         687         10         AW442233         AW442233         EST331133           1         683.8         41.2         670         12         BM400546         BST5891         AW42221         BST381163           1         674         41.0         675         12         BM400546         BM40546         BST582811 <t< td=""><td>ST58486</td><td>1053</td><td>1053</td><td>12</td><td>w</td><td>œ</td><td>30.</td><td>22</td></t<>	ST58486	1053	1053	12	w	œ	30.	22
5 742 45.4 742 12 BM413282 BM413282 BST58760 7 738 45.1 749 12 BM413075 7 726.4 44.4 728 12 BM413075 7 726.4 44.4 728 12 BM413075 8 709 43.3 729 10 AW222257 9 707.4 43.2 709 10 AW42253 0 694.4 42.4 696 10 AW42253 1 683.8 41.8 687 10 AW42253 1 673.8 41.2 703 12 BM336089 1 674 41.2 703 12 BM336089 1 673.8 41.2 677 10 AW42241 2 677 10 AW42241 3 673.8 41.0 675 12 BM408546 4 670.2 41.0 675 12 BM408546 6 657.2 40.2 677 10 AW42263 7 654.4 40.0 672 10 AW221785 6 657.2 40.2 678 10 AW2221785 6 657.2 40.2 679 10 AW221785 6 657.2 40.2 679 10 AW221785 6 657.2 40.2 679 10 AW221785 6 657.2 40.2 679 12 BM41547 6 659 12 BM41548 6 689 12 BM41548 6 689 12 BM41548 6 689 10 AW422380 6 AW4422880	ST40557	3449	3449	10	Ü	8	w	21
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM41343         BM41343         EST58767           7         726.4         44.4         728         12         BM413075         BM413343         EST58740           7         726.4         44.4         728         12         BM413075         BM413934         BM413075         EST58740           7         726.4         43.3         729         10         AW222257         AW222257         BM222257         EST2996           8         709         43.3         729         10         AW442253         AW442239         BST31133           9         707.4         43.2         709         10         AW442253         AW442235         BST311134           9         694.4         42.4         696         10         AW442253         AW442235         BST31173           1         683.8         41.8         687         10         AW442233         AW442235         BST31173           2         674         41.2         703         12         BM536089         BST58911           3         673.8         41.2         673         10         AW42	ST31167	4228	4228	10	w	9	w	20
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM41343         BM41343         BM41343         BST58767           7         726.4         44.4         728         12         BM413075         BM413343         BST587870           7         726.4         44.4         728         12         BM413075         BM413075         BST58740           8         709         43.3         729         10         AW222257         AW222257         BST29966           9         707.4         43.2         709         10         AW442339         AW4412939         BST311133           0         694.4         42.4         696         10         AW422253         BST311133           1         683.8         41.8         687         10         AW42233         AW442235         BST311133           1         683.8         41.2         673         12         BM498241         AW422241         BM536089         BST58911           1         673.1         41.2         677         10         AW442241         AW442241         BST381163           4         670.2         41.0         675         12 <t< td=""><td>ST31144</td><td>44205</td><td>4205</td><td>10</td><td>4</td><td>٥</td><td>42.</td><td>19</td></t<>	ST31144	44205	4205	10	4	٥	42.	19
5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         BM413343         BM413343         BST58760           7         7.2.6.4         44.4         728         12         BM413075         BM413343         BST58740           7         7.2.6.4         44.4         728         12         BM413075         BM413075         BM413075         BM413075         BST58740           7         7.2.6.4         44.4         728         12         BM413075         BM413075         BM413075         BM222257         BST29906           8         70.7.4         43.2         70.9         10         AW422257         BST391133         BM43233         BST311133         BST311133         BST311133         BM442233         BST311133         BM442233         BST311133         BM442233         BST311133         BM536089         BST3891113         BM536089         BST381133         BM442241         BM536089         BST31123         BM442241         BM442241         BST31123         BM442241         BM442241         BM442241         BM442241         BST38183         BM408546         BST38183         BM408546         BST38891         BM408546         BST28899         BM408546         BST	ST30021	2340	2340	10	4	9	4	18
5 742 45.4 742 12 BM413282 BM413282 BST58767 7 726.4 44.4 728 12 BM413075 BM413343 SST58767 7 726.4 44.4 728 12 BM413075 8 709 43.3 729 10 AW222257 9 707.4 43.2 709 10 AW442939 9 707.4 43.2 709 10 AW442939 9 707.4 43.2 709 10 AW44293 9 8ST311133 694.4 62.4 696 10 AW44233 10 683.8 41.8 687 10 AW44233 11 683.8 41.2 677 10 AW44233 11 683.8 41.2 677 10 AW442241 12 677 10 AW442241 13 673.8 41.2 677 10 AW442241 14 675 12 BM408546 15 657.2 40.2 670 12 BM411547 15 657.2 40.2 670 10 AW222222 16 674 40.2 670 10 AW222222 17 674 40.2 670 10 AW222222 18 674 675 12 BM408546 18 68758887	ST29859	2178	W22178	10	~1	0	54.	17
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5         742         45.4         742         12         BM413282         BM413282         BM413282         BM413282         EST58767           7         726.4         44.4         728         12         BM413075         BM413073         BM413043         EST58740           7         726.4         44.4         728         12         BM413075         BM413075         BM413075         EST58740           8         709         43.3         729         10         AW222257         AW222257         EST29906           9         707.4         43.2         709         10         AW442339         AW441939         EST31133           0         694.4         42.4         696         10         AW42253         EST31173           1         683.8         41.8         687         10         AW42233         AW42233         EST31173           1         683.8         41.2         670         12         BM40824         BM536089         BST5809           3         673.4         41.2         677         10         AW442234         BM408246         EST31163           4         670.2         41.0         675         12         BM408246         BM408	ST58587	1154	M41154	12	~1	0	57.	15
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5     742     45.4     742     12     BM413282     BM413282     BM413282     BM413343       738     45.1     749     12     BM413343     BM413343     BM413343     EST5878767       7     726.4     44.4     728     12     BM413075     BM413075     BM513075       8     709     43.3     729     10     AW222257     AW222257     EST29906       9     707.4     43.2     709     10     AW441939     AW441939     BST31133       9     694.4     42.4     696     10     AW442253     AW442253     BST31173       1     683.8     41.8     687     10     AW442335     AW442335     AW442335     BST31173       2     674     41.2     703     12     BM536089     BM536089     BM536089     BM536089	ST31163	4224	W44224	10	~1	۲	73.	13
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	ST58760	1328	1328	12		Ü	•	ហ

## ALIGNMENTS

COMMENT	TITLE JOURNAL	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BM410796 LOCUS DEFINITION
Contact: CUG1 Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics Institute	Isal, J., Bougri, C., KIKHESS, B., ULTERDACK, T., Van AKEN, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.  Generation of ESTs from tomato fruit tissue, breaker stage (2002) Unpublished (2002)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.  1 (bases 1 to 797)  Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tesai J. Paveri O. Virbeec F. Utterback T. Var aken G.	EM410796.1 GI:18262426 EST: Lycopersicon esculentum (tomato) Lycopersicon esculentum	BM410796 797 bp mRNA linear BST 22-JAN-2002 EST585123 tomato breaker fruit Lycopersicon esculentum cDNA clone

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                                  AAATGGAGTTAGGATCAAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACATCAAATT 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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EST587144 tomato breaker fruit L
CLEG61A20 5' end, mRNA sequence.
BM412817
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                         AAAAACAAGAATTAICTTCTCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATT
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                                                                                 AAAAACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATT
                                                                                                                                                                  TTTCCGCAAGCATGGAAGCATGTTCATCTAGAACACCTGTTCAATTTGTGGTTCCT
                                                                                                                                                                                                         TTTGAGCAAGCATGGAAGCATGTTCATCTAGAACACCTGTTCAATTTGTGGTTCCT
  TCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTACAAAGATAGA
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                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                  /note="Wector: pBluescriptSKmcUadapt; Site 1: EcoR1; Site 2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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/clone="cLEG61A20"
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/cultivar="TA496"
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Pred. No. 6.3e-119;
0; Mismatches 10;
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 Unpublished (2002)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
Institute
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                     BM412528 767 bp
EST586855 tomato breaker fruit I
CLEG6014 5' end, mRNA sequence.
BM412528
BM412528.1 GI:18264158
                                                                                                                                                                   Giovannoni, J.
                                                                                                                                                                                 Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon.
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Lycopersicon esculentum
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/clome="cLEG6014"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="GOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clome lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmCUdadapt; Site_1: EcoR1;
Site_2: XhoI, supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
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/cultivar="TA496"
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Pred. No. 3.7e-118;
0; Mismatches 1;
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cLEG61N6 5' end, mRNA sequence.
BM413004
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Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamidds; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 774)
1 (bases 1 to 774)
1 (bases 1, Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Blcala, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
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                                                                                                                                                                                                                                                                                                           GAAAAACATATGATAATATTGCATTTGAGCAAGCATGGAATGAAGCATGTTCATCTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTTCAAATTTGATGATCAATGCTTCAGCAAAGAGCCCAAATACTG
                                                                                                                                                 CAGGTCCATGCAGATCTTCTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTA
                                                                                                                                                                                                      CACCTGTTCAATTTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAAATCACCTTTT
                                                                                                                                                                                                                             CACCTGTTCAATTTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAAATCACCTTTT
                                                                                                                                                                                                                                                                                      GAAAAACATATGATAATATTGCATTTGAGCAAGCATGGAATGAAGCATGTTCATCTAGAA
TTGTTGGAGGAGGAGCAACTATCAATGGCAATGGACAAGTATGGTGGCCAAGTTCTTGCA
                                                                                AAATTTCAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTTCAAAATTTAG
                                                                                                                          CAGGTCCATGCAGATCTTCTATTTCAGTAAAGATTTTTTGGATCCTTAGAAGCATCTAGTA
                                        AAATTTCAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTTCAAAATTTAG
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmcUdadpt; Site_1: EcoR1;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
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/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="TA496"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
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99.2%;
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Pred. No. 3e-116;
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Generation of BSTs from tomato fruit tissue,
Unpublished (2002)
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                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                          Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
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                                                                                                                                                                                                        Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
Institute
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                                                                                                                                                                                       primer: T3
                                                                                                                                                                    Location/Qualifiers
  /tissue_type="Pericarp"
/dev_stage="breaker"
                                            /clone="clEG62H8"
                                                                                      /mol_type="mRNA"
/cultivar="TA496"
                                                                                                                          organism="Lycopersicon
                                                                   db_xref="taxon:4081"
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EST 22-JAN-2002

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RESULT 6
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BM413343 749 bp
EST587670 tomato breaker fruit
cLEG63C11 5' end, mRNA sequence
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                                                                                                                                                                                                                                                          TAACCTTCTGGAATTGCAAAAATTTGAAAGTGAATAATCTAAAGAGTAAAAATGCACAAC
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/clone lib="tomato breaker fruit"
/clone lib="tomato breaker fruit"
/clone="Wector: pBluescriptSKmcUadapt; Site_1: EcoRl;
/note="Wector: pBluescriptSKmcUadapt; Site_1: EcoRl;
/site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fru.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 749)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giovannoni,J.
Generation of ESTs
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon
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CATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTGAAAGTGAATA
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                                                   CTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTACAAAG
                                                                                                                                                                                                                                                                                     CTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTACAAAG
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/rote="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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Pred. No. 1.4e-113;
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                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.

Generation of ESTs from tomato fruit tissue, breaker stage (20 Unpublished (2002)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 728)
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                                                                                                                                                                                                                                                                                                                                                                primer: T3.
      were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the perioarp."
                                                                               /clone lib="tomato breaker fruit"
/note="Yector: pBluescriptSKmCTadapt; Site_1: EcoR1;
/note="Yhof; supplier: Boyce Thompson Institute;
// Site_2: Xhof; supplier: Boyce Thompson Institute;
// sequencing: The Institute for Genomic Research. Fru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       728 bp mRNA tomato breaker fruit Lycopersicon 5' end, mRNA sequence
                                                                                                                                                              /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                              organism="Lycopersicon/mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                        /db_xref="taxon:4081"
/clone="cLEG62K21"
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freezing the pericarp.
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                      Lycopersicon esculentum

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                        AW222257 729 bp
EST299068 tomato fruit red ripe,
                                                                                                                                             AW222257.1
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                                                                                                    Lycopersicon esculentum (tomato)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TATAGCAGATATGATATATCACAATAAACAAATCTATATCTATGTATTGAATAATTATTA 1506
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5 prime sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                        ACGTGCAAAAATGTCCATTTTAACAATGCTGAACATGTTACACCACACTGCACTTCACTA
                                                                                                   GAAGGAATTATAATGGAGAATATAAATTTAGTAGGGGAAAAGTGGAAAACCATCAGAGGCT
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                                                                                                                                                                                       AAGGGCACAAGTGCAACAAAGGTGGCCATAAAATTTGATTGCAGCACAAACTTTCCATGT
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                                                                            GAAGGAATTATAATGGAGAATATAAATTTAGTAGGGGAAAGTGGAAAACCATCAGAGGCT
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/tissue type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/dlone lib="tomato fruit red ripe, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe), 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4081"
/clone="cleN7018"
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Pred. No. 9.7e-109;
0; Mismatches 5;
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Generation of ESTs
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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EST311335 tomato fruit red ripe,
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/dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/clone lib="tomate fruit red ripe, TAMU"
/clone lib="tomate fruit red ripe, Site_1: EcoR1; Site_2:
/fincte="vector: pBlueScript SK(-); Site_2: EcoR1; Site_
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/clone="cLEN19E19"
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                                                     100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
                                                                                        Contact: CUGI
Clemson University Genomics Institute
Clemson University
                                                                                                                                        Giovannoni,J.
Generation of ESTs from Unpublished (1999)
                                                                                                                                                                                 1 (bases 1 to 696)
Alcala, Vrebalov, J., White, R., Matern, A.L., Holt, I.E.,
Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S.,
Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                                                                                                                                  Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                   AW442253 696 bp mRNA linear EST 18-MAY-200: EST311649 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                            AW442253
AW442253.1 GI:6977504
                                                                                                                                                                                                                                                                                                                                                    clone cLEN22G14 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTGGAAAACCATCAGAGGCTACGTGCAAAAATGTCCCATTTTAACAATGCTGAACATGT 1363
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1. .696
/organism="Lycopersicon esculentum"
                                       Location/Qualifiers
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                                                                     TCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGC
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Query Match 42.4%;
Best Local Similarity 99.9%;
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TCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGC
                                                                                                               TAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTACTGTAAATGAAGCCAAAATTA 1008
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/clone lib="tomato fruit red ripe, TAMU"
/clone lib="tomato fruit red ripe, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Khol; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
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/cultivar="TA496"
/db_xref="taxon:4081"
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Pred. No. 2.7e-106;
0; Mismatches 1;
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Best Local Similarity
Matches 685; Conserv
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1 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
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AW442335.1 GI:6977586
EST.
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EST311731 tomato
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                                                                                                                                                 GGCTTTGGATTGCTTTTTGATAGTGTTCAAAATTTAGTTGTTGGAGGAGGAGGAACTATCA
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="red ripe (7-20 days post-breaker)"
/clone lib="tomato fruit red ripe, TAMU"
/clone lib="tomato fruit red ripe, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="Vector: pGlueScript SK(-); Site_1: EcoR1; Site_2:
xhol; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon
/mol_type="mRNA"
/cultivar="TA496"
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 1.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
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100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giovannoni,J.

Generation of ESTs from tomato fruit tissue, breaker stage (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST589111 tomato breaker fruit I cLEG71124 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
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                    /clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSMcUadapt; Site_1: EcoR1;
Site_2: XhOI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                            /mol
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/dev_stage="breaker"
/lab_host="SOLR"
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/mol_type="mRNA"
/cultivar="TA496"
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                                                                     Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Lycopersicon.

1 (bases; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases; to 677)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S.,
Upton, J., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
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EST311637 tomato fruit red ripe, T
                                                    Giovannoni, J.
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AW442241.1 GI:6977492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGCAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAA
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Pred. No. 6.8e-103;
0; Mismatches 0;
                                 tomato
                                 fruit tissue
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TAMU Lycopersicon esculentum cDNA
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCACTAATGTTGTAGCTTCAAATTTGATGATCAATGCTTCAGCAAAGAGCCCAAATACT 794
AGTGCAACAAAGGTGGCCATAAAATTTGATTGCAGCACAAACTTTTCCATGTGAAGGAATT
                                                                                               ATACAACAGTTTTCAGCAGTTCAAGTGAAAAATGTGGTGTATGAGAAATATCAAGGGCACA 1214
                                                                                                                                                                                             CAAGACGTTAAGTATCCCATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGT
                                                                                                                                                                                                                                                                                     AAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGGAAATG
                                                                                                                                                                                                                                                                                                                                                                                GTGTCTAATGTTAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATC 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAAAGTGAATAATCTAAAGAGTAAAAATGCACAAATTCATATCAAATTTGAGTCA 734
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                                                                                                                                                                                                                                                             AAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGAGTCCATGTATCAAATACTCAATATATTCAAATATCTGATACTATTATTGGAACA 854
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/dev_stage="red_ripe (7-20 days_post-breaker)"
/clome_lib="tomato_fruit_red_ripe, TAMU"
/clome_lib="tomato_fruit_red_ripe, TAMU"
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/clome_lib="tomato_fruit_red_ripe, TAMU"
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e sequence.
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/cultivar="TA496"
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Pred. No. 7.4e-103;
0; Mismatches 2;
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatoghyta; Magnollophyta; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
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Generation of ESTs from tomato fruit tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Romning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq
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Clemson University Genomics Institute
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                                                                                                                                                                                                                                     TTCATCTAGAACACCTGTTCAATTTGTGGTTCCTAAAAAACAAGAATTATCTTCTCAAGCA
                                                                                                                                                      AATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAGTAAAGATTTTTTGGATCCTTAGA
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                  TCAAAATTTAGTTGTTGGAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCC
                                                                                            AGCATCTAGTAAAATTTCAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGT
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                                                          AGCATCTÄGTAAAATTTCAGÄCTACAAÄGATÄGÄAGGCTTTGGATTGCTTTTGATÄGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescriptSKmCUadapt; Site 1: EcoR1; Site 2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fru
                                                                                                                                                                                                                                                                                                                                                                                   were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="TA496"
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clone="cLEG45C7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="Pericarp"
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                                                                                                                                                                                                                                                                                                           41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    670 bp
EST585874 tomato breaker fruit
cLEG57K1 5' end, mRNA sequence.
EM411547
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Generation of ESTs
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1 (bases 1 to 670)
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                                                                                                                                                                                                                                 Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
Contact: CUGI
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Lycopersicon esculentum
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/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                        /db_xref="taxon:4081"
/clone="cLEG57K1"
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/cultivar="TA496"
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EST 22-JAN-2002

660

600 958 540 868 838

480

778

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360

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Query Match
Best Local Similarity 98.8
Matches 662; Conservative
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                                               CAAAAATTTG 677
                                                                                                                                 CAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTG 667
                                                                                                                                                                                                                                   AGTTGTTGGAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCAAGTTCTTG 607
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CANATATTTG 670
                                                                                                 CAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmcUdadapt; Site 1: EcoR1;
Site 2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
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Pred. No. 4.4e-100;
0; Mismatches 8; Indels 0;
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Search completed: July 27, 2004, 02:46:01 time : 4445 secs

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Maximum Match 100%
Listing first 45 summaries
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08-290-978A-5
US-09-787-583-2
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US-08-61-062A-6
US-08-61-062A-6
US-08-536-150-6
US-08-647-023-188
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APPLICANT: BRIDGES, IAN;SCHUCH, WOLL
TIPLE OF INVENTION: RECOMBINANT DNA
ESTERASE GENE SEGEMENTS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/24,866
APPLICATION NUMBER: US/08/24,866
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 720,629
PILING DATE: 25-JUN-1991
APPLICATION NUMBER: 419,779
PILING DATE: 29-SEP-1989
APPLICATION NUMBER: 119,614
PILING DATE: 12-NOV-1987
IQ ID NO:1:
LENGTH: 457
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                                                      ASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSL
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; OTHER INFORMATION: Strain cv. US-09-051-239A-2
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Best Local S
Matches 223
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SEQ ID NO 2
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Patent No. 6420628
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APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/EP96/04313
PRIOR FILING DATE: 1996-10-04
PRIOR APPLICATION NUMBER: EP 95 402241.4
PRIOR APPLICATION NUMBER: EP 96 402241.4
PRIOR FILING DATE: 1995-10-06
PRIOR FILING DATE: 1995-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2121-0138P
CURRENT APPLICATION NUMBER: US/09/051,239A
CURRENT FILING DATE: 1998-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BOTTERMAN, Johan TITLE OF INVENTION: Seed Shattering FILE REFERENCE: 2121-0138P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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TYPE: PRT
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                                IIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINL 415
                                                                                                                                                                          NLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGI
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IIDQNYCDK-DKCEQQESAVQVNNVVYQNIKGTSATDVAIMFNCSVKYPCQGIVLENVNI
                                                                              SIGSLGDDNSKAYVSGIDVDGATLSETDNGVRIKTYQGGSGTAKNIKFQNIRMDNVKNPI
                                                                                                              SIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPI
                                                                                                                                                    NVKITAPGDSPNTDGIHIVATKNIRISNSDIGTGDDCISIEDGSQNVQINDLTCGPGHGI
                                                                                                                                                                                                                                  GNGNIWWQNSCKIDKSKPCTKAPTALTLYNLKNLNVKNLRVRNAQQIQISIEKCNNVGVK 231
                                                                                                                                                                                                                                                        GNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVAS 235
                                                                                                                                                                                                                                                                                                            YLLKSIRFRGPCKSLRSFQILGTLSASTKRSDYSNDKNHWLILEDVNNLSIDGGSAGIVD
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BORKHARDT, Ber
SANDER, Lilli
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                                                                                                                                                                                                                                                                                                                                                YLLKQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGG--GTIN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVFLCVLLMLACCQALSSNV-DDG-----YGHEDG---SFESDSLIKLNNDD
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VAN ONCKELIN, Henri
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BUNDGARD POULSEN, Gert
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Pred. No. 2.2e-92;
9; Mismatches 121;
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US-08-941-532-6
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US-08-941-532-6
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/GB96/00757
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 9
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROBERTS, Jeremy Alan
APPLICANT: COUPE, Simon Allan
APPLICANT: JENKINS, Elizabeth Sarah
TITLE OF INVENTION: CONTROL OF POD
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                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/941,532 FILING DATE: 30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                      KIWWQNSCKIDKSKPCTKAPTALTLYNLNNLNVKNLRVRNAQQIQISIEKCNSVDVKNVK 234
                                                    QVWWPSSCKINKSLPCRDAPTALITEWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLM 238
                                                                                                                                                                                                                                                    AIFICVLLMLACCQALSSNVDDGYGHEDGSFET--DSLIKLNNDDDVLTLKSSDRPTTES
                                                                                                                                                                                                                                                                                          SILLLIIIFASSISTCRSNVID-----DNLFKQVYDNILEQEFAHDFQAYLSYLSKNIES 61
                                                                                                KSIRFRGPCKSLRSFQILGTLSASTKRSDYSNDKNHWLILEDVNNLSIDGGSAGIVDGNG 174
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1100 New York Avenue
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                                                                                                                                                                                                                                                                                                                                Conservative
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RESULT 4
US-08-467-023-134
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                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-467-023-134
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                             Query Match
Best Local Similarity
Matches 168; Conserv
                                                                                                                                                                                               TELEFAX: (617) 227-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                           REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS: ImmuLogic Pharmaceutical Corporation,
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/350,225 FILING DATE: December 6, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08, FILING DATE: June 6, 1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                TYPE: amino acid
                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                 NAME: Jane E. Remillard
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AHDFQAYL---SYLSKNIESNNNIDKVD---KNGIKVINVLSFGAKGDGKTYDNIAFEQA
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Bond, Julian F.;
Garman, Richard D;
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Exley, Mark A.;
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuo, Mei-Chang;
Yeung, Siu-mei H.;
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                                                32.9%;
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                                                                                                                                                                                                   134:
                                  73;
                                                                                                                                                                                                                                                                  025.6 USD2 (IMI-028CPD2)
                                Score 787; DB 3;
Pred. No. 9.1e-63;
3; Mismatches 160
                                  160;
                                                              Length 514;
                                  Indels
                                  14;
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412
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;Patent No.
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                                                                                                                                                                                                                                                                      US-08-467-023-189
                                                                                                                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; APPLICANT: SHEWMAKER, CHRISTINE K.; KRIDL, JEAN C.; HIATT, WILLIAM R.; KNAUF, VIC ; TITLE OF INVENTION: ANTISENSE REGULATION OF GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;SEQ ID NO:2:
                                                                                                                                                                                              Sequence 189, Application US/08467023 Patent No. 6090386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                             GENERAL INFORMATION:
APPLICANT: Griffe
APPLICANT: Polloc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 27-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         applicant: SHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 240,408
FILING DATE: 30-AUG-1988
APPLICATION NUMBER: 920,574
FILING DATE: 17-OCT-1986
APPLICATION NUMBER: 845,676
FILING DATE: 28-MAR-1986
                            APPLICANT:
                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 SSISVKIFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 QLKCSDSMPCKDIKLSDISLKLTSGK--IASCLNDNANGYFSGHVIPACKNLSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 GTGSSNIVIEDLICGFGHGISIGSEGRENSRAEVSYVHVNGAKFIDTQNGLRIKTWQGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 VSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 AEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFNVEKYGAVGDGKHDCTBAFSTA
                                                                                                                                                                                                                                                                                                                                                                                                              61 SSISVKIFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 WQAACKNPS-AMLLVPGSKKFVVNNLFFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTFVQFVVPKNKNYLLKQITFSGPCR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMASHIIYENVEMINSENPILINQFYCTSASACQNQRSAVQIQDVTYKNIRGTSATAAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Solitarity 100.0%; Figure 100
                                                                                             Griffeth, Irwin Pollock, Joanne;
                            Garman,
Kuo,
                                                             Bond, Julian F.;
Mei-Chang;
                            Richard
                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                 Irwin J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     %; Score 365; DB
%; Pred. No. 7.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 70
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RESULT 7
US-09-107-532A-6652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                    Sequence 6652, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350

FILING DATE: December 6,

ATTORNEY/AGENT INFORMATION:

NAME: Jane B. Remillard

REGISTRATION NUMBER: 38,87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Allergenic Proteins And Peptides TITLE OF INVENTION: Japanese Cedar Pollen NUMBER OF SEQUENCES: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08, FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 610 Li
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                               293 HGISIGSIGSGNSEAYYSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFINVEMQDVK 352
                                                                                                                                                                                                                                                                                                                                                                          353 YPIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGI 408
                                                                                                                                                                                                                                                                                                                                            68 NPILINQEYCTSASACQNQRSAVQIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDI 123
                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                                   STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                            HEFSIGSLGRENSRAEVSYVHVNGAKFIDTQNGLRIKTWQGGSGMASHIIYENVEMINSE
                                                                                      CITY: Waltham
                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Powers, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brauer, Andrew;
Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeung, Siu-mei H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ImmuLogic Pharmaceutical Corporation,
                                                                                                      100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%;
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ER: 025.6 USD2 (IMI-028CPD2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 319; DB 3; Length 127; Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version
                                                                                                                                                                        and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEU'
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                                                                                                                                                                         AND THERAPEUTICS
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                                                                                   RESULT 8
US-08-290-978A-5
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Sequence 5, Application US/08290978A
Patent No. 5624834
GENERAL INFORMATION:
APPLICANT: KUSTERS-VAN SOMEREN, MARGO
APPLICANT: MULLER, YVONNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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US-09-107-532A-6652
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Artiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...451
SEQUENCE DESCRIPTION: SEQ ID NO: 6652:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
344 HASA 347
                                                     386 KGTS 389
                                                                                                                                                                               341 IKFLNVEMQDVKYPIIIDQNY-CD--RVEPCIQQ---
                                                                                                                                                                                                                                                                                             282 VQATNITCGPGH-GISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 NGKKWWHTFRNEPD----NLAYP---RPKLMSFHNCHRITVKDIKLIQSPSWTINPILCS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 SISVKIFGSLEASSKIS-DYKD-------RRLW---IAFDSVQNLVVGGGGTING 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 KSNVELHLSAGAVLKFSDDPKDYPVVHSRWEGVHRKVYASCIYAQNVENISVTGFGTLDG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 IKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 12.5%; Score 299; DB 4; Similarity 27.2%; Pred. No. 1.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                  NVVASNIMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGS-----QN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INMYDILTEGASID--ELNTEAIQQAIDAAASDGGGT-VVVPAGE-----FLTGALFL 54
                                                                                                                          IRVSNIVMDNVMCPFILNLYYFCGPRGKEPYVWEKKAYPIDERTPAFRRIHFSNITARNV
                                                                                                                                                                                                                                        ITITNCTMVHGHGGVVLGSEMSGS----IRNITISNCIFQETDRGIRLKSRRGRGGIVED 283
                                                                                                                                                                                                                                                                                                                                                            NATFONLTILNPADSPNTDGIDPESCKNVRISNCHIDVGDDCIAIKAGTEDTYERIACEN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGQVWW-----PSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (781)893-50
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: PC
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443 LSVNCTA 449

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US-08-290-978A-5
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Best Local :
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 46:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/290,978A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CLONING AND EXPRESSION OF THE TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS NUMBER OF SEQUENCES: 15
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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TOPOLOGY: linear
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TELEFAX: (202) 887-0763
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VIPHCIS
                                                                                 KGTSA-----TKVAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEH 437
                                                                                                                                                                                                            GSLGQYKDEVDIVENVYVYNISMFNASVCLNFNHIIDFLLTWLQDMARIKVWPGTPSALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKNIDLEVLGTILFTNDTDYWQANSFKQGFQNATTFFQLGG-EDVNMYGGGTINGNGQVW
                                           RGTTSGSEDPYVGTIV---
                                                                                                                      ADLQGGGGSGSVKNITYDTALIDNVDWAIEITQCYGQKNTTLCNEYPSSLTISDVHIKNF
                                                                                                                                                                -----GGSGQASNIKFLNVEMQDVKYPIIIDQNYCDR-VEPCIQQFSAVQVKNVVYENI 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTCHVRSHGDGTDDSDYILSALNQ-----CNHGGKVVF--DEDKEYIIGTALNMTF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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  444
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; Pred. No. 1.3e-18;
73; Mismatches 166;
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                                         CSSPDTCSDIYTSNINVTSPDG-TNDFVCDNV---DESL
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                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 90-4030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08,
FILING DATE: 24-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 17-OCT-1994
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006-1812
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MURASHIGE, KATE REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                           Match 12.5%;
Local Similarity 25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                   212
                                                                                                    156 YDLYAEDDLIL----RPILMGIIGLNGGTIGPLKLRYSPQYYHFVANSSNVLFDGIDISG
                                                                                                                                                                                                      131 RSSISVKIFGSL-----EASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVW 181
                                                                                                                                                                                                                                         48
                                                                                                                                                                  97 LKNIDLEVLGTILFTNDTDYWQANSFKQGFQNATTFFQLGG-EDVNMYGGGTINGNGQVW 155
                                                                                                                                                                                                                                                                       74 KVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLL---KQITFSGPC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Application US/08780869 5830737
                                   YSKSDNEAKNTDGWDTYRSNNIVIQNSVINNGDDCVSFKPNSTNILVQNLHCNGSHGISV
                                                                 SAKS----PNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISI 297
                                                                                                                                  WPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA 241
                                                                                                                                                                                                                                       KTCHVRSHGDGTDDSDYILSALNQ-----CNHGGKVVF--DEDKEYIIGTALNMTF----
     GSLGSGNSE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                              452 amino acids
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                                                                                                                                                                                                                                                                                                           Conservative
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     - AYVSNVTVNEAKI IGAENGV--
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                                                                                                                                                                                                                                                                                                         Score 298.5; DB 2;
Pred. No. 1.3e-18;
3; Mismatches 166;
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                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                           Length 452;
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; Sequence 1, Application US/09542767A; Patent No. 6296671
                                            US-09-542-767A-1
                                                                 RESULT 11
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; ORGANISM: Aspergillus tubingensis
US-09-787-583-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09787583 Patent No. 6602696 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VOTAGEN, Alphons
TITLE OF INVENTION: ASPERGILLUS TUBIGENSIS POLYGALACTURONASE
FILE REFERENCE: 24615-20144.00
CURRENT APPLICATION NUMBER: US/09/787,583
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: EP 99200481.2
PRIOR PILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: EP 98203171.8
PRIOR FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                         318 SSGTDIYIL--CGSG-SCSNWTWSGVDVTG--GKKS-SKCKNV 354
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                                                                                                                                                                                                                                                                              CLAINSG-EHITFTNGYCDGGHGLSIGSIG-GRSDNTVNDVTISNSKVLNSQNGVRIKTI
                                                                                                                                                               TSATKVAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNV 430
                                                                                                                                                                                                     YGKTGTVENVKFEDITLSDISKYGIVVEQDY-ENGSPTGTPTNGVKVEDITFKKVTGSVK
                                                                                                                                                                                                                                                                                                                          CISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTW 331
                                                                                                                                                                                                                                                                                                                                                                                                        QQIHIKFESCTNVVASNLMIN-----ASAKSPNTDGVHVSNTQYIQISDTIIGTGDD
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                                                                                                                                                                                                                                                                                                                                                                -----FSILADHĹTITDVTIDNSAGTSKGHNTDAFDIGQSTYITIDGATVYNQDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herweijer, Margareta
Meeuwsen, Petrus
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Grassin, Catherine
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Pred. No. 2.6
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nes 91;
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US-08-061-062A-6
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CURRENT FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: PA 1999 00390
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 60/125,884
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: PCT/DK00/00136
PRIOR APPLICATION NUMBER: PCT/DK00/00136
PRIOR FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08061062A Patent No. 5550045
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APPLICANT: Kristensen, Henrik
TITLE OF INVENTION: An Enzymatic Treatment Method
FILE REFERENCE: 5871.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn vers
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                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                           APPLICANT: VERBAKEL, Johannes M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA
TITLE OF INVENTION: ENCODING A RIPENING FORM OF A
TITLE OF INVENTION: RHAMNOGALACTURONASE ACTIVITY
NUMBER OF SEQUENCES: 16
                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Disk
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                                                                                                                                                                           STREET: 1100 NEW Y
                                                                                                                                                             COUNTRY:
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APPLICATION NUMBER:
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                                                                                                                                          20005-3918
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                                                                                                                                                             U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                        STAM, HEIN
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US/08/061,062A
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                                         Version
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#1.25

POLYPEPTIDE HAVING

DB 3;

Length 360; Indels

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                                                                                                                                                                                                                                                                                  Patent No. 5550045
GENERAL INFORMATION:
APPLICANT: MUSTERS, WOUTER
APPLICANT: STAM, HETM
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acid
                                                                                                                                                                              APPLICANT: VERBAKEL, Johannes M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA
TITLE OF INVENTION: ENCODING A RIPENING FORM OF A POLYPEPTIDE HAVING
TITLE OF INVENTION: RHAMNOGALACTURONASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE JOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM: MEDIUM TYPE: Disk
                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                          ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON, D.C.
                                        ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                           COUNTRY: U.S.A.
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Best Local
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                                  TITLE OF INVENTION: CLO
TITLE OF INVENTION: ENC
TITLE OF INVENTION: RHA
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 1677
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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STREET: 1:
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TELEFAX: (202) 822-0944
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                                                                           VERHAKEL, JOHANNES M.
VERTION: CLONING AND EXPRESSION OF DNA
VENTION: ENCODING A RIPENING FORM OF A
VENTION: RHAMNOGALACTURONASE ACTIVITY
                                                                                                                                                       SUYKERBUYK, MARIA E. VISSER, JACOB
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TELEX: (6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino
                                                        Sequence 8, Application US/08536150 Patent No. 6013489
GENERAL INFORMATION:
APPLICANT: MUSTERS, WOUTER
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     APPLICANT:
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MUSTERS, WOUTER
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VISSER, JACOB
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Pred. No. 2e-13;
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/061,062
FILING DATE: 14 MAY 1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VERBAKEL, Johannes M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA
TITLE OF INVENTION: ENCODING A RIPENING FORM OF A POLYPEPTIDE HAVING
TITLE OF INVENTION: RHAMNOGALACTURONASE ACTIVITY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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Local Similarity 24.0%; Pred. No. 2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 NEW Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 29-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Disk
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366 YLCRSAY 372
                                           425 ATCKNVH 431
                                                                                                                                    368 CIQQFSAVQVKNVVYENIKGT---SATKVAIKFDCSTNFPCEGIIMENINLVGESGKPSE 424
                                                                                                                                                                               250 DVTDIVYRNVYTWSSNOMYMIKS-NGGSGTVSNVLLENFIGHGNAYSLDIDGYWSSMTAV 308
                                                                                                                                                                                                                           308 YVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEP 367
                                                                                                                                                                                                                                                                             194 LDGIDVWGSN-IWVHDVEVTNKDECVTVKSPANNILVESIYCNWSGGCAMGSLG---ADT 249
                                                                                                                                                                                                                                                                                                                      248 TDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEA 307
                                                                                                                                                                                                                                                                                                                                                                       144 GARILRLTDV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 CRSSISVK--IFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCK 187
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                                                                                      A---GDGVQLNNITVKNWKGTEANGATRPPIRVVCSDTAPCTDLTLEDIAIWTESGSSEL 365
                                                                                                                                                                                                                                                                                                                                                                                                                  INKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SATAIQLDGIIYRTGTÄSGNMIAVTDTTDFELFSSTSK-----GAVQGFGYVYHAEGTY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGATKTCNILSYGAVADNSTDVGPAITSAW-AACKSGGLV--YIPSGNYALNTWVTLTGG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 amino acids
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Job time : 29.379 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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110:
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Gapop 10.0 , Gapext 0.5
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2390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published
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Copyright (c) 1993 - 2004 Compugen Ltd.
/ Cgn2_6/ptodata///pubpaa/US08_NEW_PUB.pep:*
/ Cgn2_6/ptodata//pubpaa/US08_PUBCOMB.pep:*
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_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Result No.
1011 1010 9887 870 808 787.5 785 739 734 728 724.5 723.5 701.5	Score
	Query Match Length DB 46.6 433 1
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US-10-437-963-127090 US-10-437-963-127091 US-10-437-963-131044 US-10-425-114-69361 US-10-425-114-69361 US-10-437-963-154485 US-10-437-963-175508 US-10-437-963-172689 US-10-437-963-172689 US-10-424-599-235443 US-10-424-599-235443 US-10-425-114-4707 US-10-424-599-284649 US-10-424-599-284649 US-10-437-963-155040	ID
Sequence 127091, Sequence 127091, Sequence 127091, Sequence 131044, Sequence 6361, A Sequence 696, Appl Sequence 134257, Sequence 172689, Sequence 172689, Sequence 235443, Sequence 44707, A Sequence 44707, A Sequence 484649, Sequence 284649, Sequence 155040,	Description

Length 433;

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627	627	627	627	627	627	627	627	627	627	630	630	630	632	635.5	641.5	642	643.5	649.5	653.5	653.5	653.5	660	•	666	7	681		699	
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416	416	415	415	415	413	413	412	410	407	414	414	410	386	539	544	320	602	449	415	411	385	422	415	393	457	737	571	496	0 / 0
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-10-425-114-7278	-10-425-114-6	US-10-425-114-64510	25-114-5	0-425-114-4	US-10-425-114-56708	0-425-114-5	25-114-4	US-10-425-114-46486	US-10-425-114-65565	0-425-	US-10-425-114-62958	0-425-114-3847	0-425-114-5098	7646	-10-437-9	0-424-599-20480	-10-437-963-12708	-10-437-963	-10-425-114-51	0-425-114	-10-425-114-4198	24-599-1763	0-424-599-23851	7-963-	37-963-14616	37-963-16	-10-437-963-15910	US-10-425-114-66151	CO-TO-#CO-TT#-#5#TO
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2785,	564,	ò	`	800,	56708,	982,	801,	•	55565,	•	`	475, A	•	6466,	110126,	4806,	127089,	$\sim$	,	,	1984, A	176320,	238512,	6114,	6	2350,	9100,	151, A	•

# ALIGNMENTS

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; OTHER INFORMATION: Strain cv. US-10-151-668-2
                                                                                                                                                                                                                                                                                         APPLICANT: BORKHARDT, Bernard
APPLICANT: SANDER, Lilli
APPLICANT: STANDER, Lilli
APPLICANT: SUNDARD POULSEN, Gert
APPLICANT: BUNDARD POULSEN, Gert
APPLICANT: BUNDARD POULSEN,
TITLE OF INVENTION: Seed Shattering
TITLE OF INVENTION: Seed Shattering
FILE REFERENCE: 2121-0138P
CURRENT APPLICATION NUMBER: US/10/151,668
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/051,239
PRIOR FILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: POT/EP96/04313
PRIOR FILING DATE: 1996-10-04
PRIOR APPLICATION NUMBER: EP 95 402241.4
PRIOR APPLICATION NUMBER: EP 95 402328.0
PRIOR APPLICATION NUMBER: EP 95 403328.0
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                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
SEQ ID NO 2
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APPLICANT:
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1995-12-08
NUMBER OF SEQ ID NOS: 14
                                                                                                                                   TYPE: PRT
ORGANISM: Brassica
                                                                                                                  FEATURE:
                                                                                                                                                                                     LENGTH: 433
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  46.6%;
49.9%;
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  Score 1113; DB 13; Pred. No. 1.8e-97;
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US-10-437-963-127090
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                                                                                                                                                                                                                                                                                                            APPLICANT: II, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(52321)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 127090
LENGTH: 393
LENGTH: 393
                                                                                                                                                     Query Match
Best Local Similarity
Matches 187; Conserv
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                     SSISVKIFGSLEASSKISDYKDR--RLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKIN
                                                                           GSNVFSIQSYGAHGDGKHDDTKALGDTWAAACSSAKPAVLLIPKGKKYLIKHTTLSGPCK
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                                                                                                         GIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVKITAPGDSPNTDGIHIVATKNIRISNSDIGTGDDCISIEDGSQNVQINDLTCGPGHGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SILLLIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNID
   SSISLMVKGSLVASPERSDWSKETIRHWILISGVTGLTVTGGGTIDGNGKIWWQNSCKTN
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Cao, Yongwei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIDQNYCDK-DKCEQQESAVQVNNVVYQNIKGTSATDVAIMFNCSVKYPCQGIVLENVNI 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGSLGDDNSKAYVSGIDVDGATLSETDNGVRIKTYQGGSGTAKNIKFQNIRMDNVKNPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV-----DKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKN 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boukharov,
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                                                                                                                                                     Conservative
                                                                                                                                                   42.3%; Score 1011; DB 16; Length 53.3%; Pred. No. 9e-88; rative 57; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrey A.
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; Sequence 127091, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_29576C.1.pep
US-10-437-963-127091
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SEQ ID NO 127091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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APPLICANT:
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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TYPE: PRT
ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                       135 SVKIFGSLEASSKISDYKDR--RLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190;
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                                                                                                                                                                                                          VSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNV 312
                                                                                                                                                                                                                                                                                                                              TEMIEGTLVAPPKRSDWSKETIRHWIMFNGVSGLTVAGGGTVDENGKIWWQNSCKTNAKL
                                                                                                                                                                                                                                                                                                                                                                                                       VFDVRKHGAYGDGQHDDTKALAKAWAAACSSSQPSIVLIPKGKRYLTKHITLSGPCKSSI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                         VINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCKSAVEVSNVLFKNIRGTSASEEAIMLHCSSSVPCHGITLENVNLTVKGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYV 309
                     SAVQVSNVVFKNIRGTSASKEAIKLDCSRNVPCQGITLKDVKLTIKGG
                                                       SAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESG
                                                                                                                                   TVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQF 372
                                                                                                                                                                        ITRSKNVQVTGCIIKTGDDCMSIEDGTENLHVKNMVCGPGHGISIGSLGDHNSEAHVNNV
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Barbazuk, Brad
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54.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1010; DB 16; Pred. No. 1.4e-87;
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With

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RESULT 5
US-10-425-114-69361
; Sequence 69361, Application US/10425114
; Publication No. US20040034888A1
; GENERAL IMPORMATION:
APPLICANT: Liu, Yihua
; APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecule
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US-10-437-963-131044
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SEQ ID NO 131044
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Best Local
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 SVKIFGSLEASSKISDYKD--RRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186;
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Cao, 1
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49.5%;
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Pred. No. 1.5e-85;
       Molecules
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     and Other
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     Molecules
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       Associated
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                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 154485
SEQ ID SERVING S
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LENGTH: 319
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Matches 173;
                                        Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: UC-ZMFLB73002C03_FLI.pep
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                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SGITIDSVQLHGTTNGARIKTYQGGSGYAKDITFQNMVMYDVKNPIIIDQNYCDKAKPCG
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Wu, Wei
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    Conservative
                                                                                                                                                                                        Clone ID: PAT_MRT4530_54340C.1.pep
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33.8%; Score 808; DB 16; 36.4%; Pred. No. 3.6e-68; tive 91; Mismatches 167;
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Pred. No. 2.1e-74;
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        167;
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        44;
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US-09-847-208-69
Sequence 69, Application US/09847208
Publication US20030082190A1
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; ORGANISM: Cryptomeria japonica (Japanese cedar)
US-09-847-208-69
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Best Local :
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LENGTH: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES FILE REFERENCE: UC67.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Saxon, Andrew APPLICANT: Zhang, Ke APPLICANT: Zhu, Daocheng
                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 173; Conserv
  167
                                       185
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                                   SCK-INKSLPC--RDAPTALTEWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
                                                                              FFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTLMGKGVIDGQGKQWWAG 166
                                                                                                                                                                                                 VD---KNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQI
                                                                                                                                                                                                                                        VAMQLIIMAAA---
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                                                                                                                    TFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPS
                                                                                                                                                           VEHSRHDAINIFNVEKYGAVGDGKHDCTEAFSTAWQAAC-KKPSAMLLVPGNKKFVVNNL
                                                                                                                                                                                                                                                                             ILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNIDK 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSKNIESNNNIDKVDKN---
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  QCKWVNGREICNDRDRPTAIKFDFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITA
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                                                                                                                                                                                                                                                                                                                   Score 787.5; DB 10;
Pred. No. 3.3e-66;
8; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 514;
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_36049C.1.
US-10-437-963-134257
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SEQ ID NO 134257
LENGTH: 534
TYPE: PRT
ORGANISM: Oryza sativa
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               141 SLEASSKISDY--KDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLPCR--D 196
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                    SLKLGNFSSLWMQTQAVEVRKIEFAGIRGTSATEQAIKLACSDAVPCRDLELRNVNLTMV
                                                                                                                                      AKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQ-----
                                                                                                                                                                                                                 QYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNE 316
                                                                                                                                                                                                                                                                                                  APTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNT 256
                                                                                                                                                                                                                                                                                                                                          TIAAPASPDEWAGRDPTKWLYVFRVDDLSVSGGGTIDGMGAEWWARSCKRKKTKPCSTVS
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Can, Yongwei
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                                                        ----FS----AVQVKNVVYENIKGTSATKVAIKFDCSTNFFCEGIIMENINLVGE 418
                                                                                                                                                                              THAQIMDNLISTGDDCVSMVGNCSDVRVKDISCGPGHGISIGSLGKNRTTDRIENVRVDT 369
                                                                                                                                                                                                                                                             APKALQFEECRRVSVQGITMQNGPQFHLMFTRCTDVKASFLRVVAPESSPNTDGIHLNDT 309
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Boukharov, Andrey
Barbazuk, Brad
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7; Mismatches 146; Indels
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Pred. No. 6.1e-66;
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Length 534;

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SGKPSEATCKNVHENNAEHVTP

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RESULT 10
US-10-437-963-172689
; Sequence 172689, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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US-10-437-963-175508
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US-10-437-963-175508
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID MOS: 204966
SEQ ID NO 175508
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Best Local S
Matches 153
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              APPLICANT:
                                                                     APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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APPLICANT:
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                                       Zhou, Yime
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Wei
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Barbazuk, Brad
            Boukharov, Andrey A.
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; Pred. No. 1.3e-61;
62; Mismatches 128;
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                                                        ; OTHER INFORMATION: US-10-424-599-235443
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-235443
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Matches
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SEQ ID NO 172689
LENGTH: 503
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 235443
Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 235443, Application US/10424599 Publication No. US20040031072A1
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                          TITLE OF INVENTION: Soy Nucleic Acid TITLE OF INVENTION: Plants and Uses FILE REFERENCE: 38-21(53223)B
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ORGANISM: Oryza sativa
                                                                                                       TYPE: PRT
ORGANISM: Glycine
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Pred. No. 4
   Score
Pred.
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   728; DB 12;
No. 1.3e-60;
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Thereof for Plant Improvement
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APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

ENG ID NO 44707

LENGTH: 456

TYPE: DDT.
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Best Local S
Matches 158
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                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: 700847226_FLI.pep-10-425-114-44707
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine
FEATURE:
                                                                                                                   119 FQLDGKIIAPTSSEAWGSGTLQWLEFSKLNTITIRGKGVIDGQGSVWWNNDSPTYNPTEV 178
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                                        179 MLESNGRLP-STKPTALRFYGSDGVTVTGITIQNSQQTHLKFDSCTNVQVSGISVSSPGD
                                                                          187 KI--NKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAK 244
                                                                                                                                                         136 VKIFGSLEASSKISDYKDRRL-WIAFDSVQNLVVGGGGTINGNGQVWW------PSSC 186
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SPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGN
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42.9%; Pred. No. 1.4e-60;
tive 51; Mismatches 139;
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US-10-362-091-4
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APPLICANT: Institute de Cincia Aplicada e Tecnologia (ICAT)
APPLICANT: Institute de Cincia Aplicada e Tecnologia (ICAT)
TITLE OF INVENTION: Pear genes codifying for b-Galactosidase, Pectin Methylesterase,
TITLE OF INVENTION: Polygalacturonase, Expansin and their use.

FILE REFERENCE: none
CURRENT APPLICATION NUMBER: US/10/362,091
CURRENT FILING DATE: 2003-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
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Best Local Similarity
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TYPE: PRT
373
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                                                                                                                                                                                                                                                                                                                                                                                                                   81 AVFSGPCKNNAITFRIAGTLVAP---SDYRVIGNAGNWLLFQHVNGVTI-SGGVLDGQGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 TKACVRNVTVRDVTIQNTLTGVRIKTWQGGSGSVQNIMFSNVQVSGVQTPISIDQYYCDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 NIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SITNVDAAAV-TFSVSSLGAKADGSTDSTKAFLSAWSNACASVNPAVIYVPAGR-FLLGN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEPCIQQFSAVQVKNVVYENIKGTSAIKVAIKFDCSTNFPCEGIIMENINIVGESGKPSE
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                                                                                                                                                                   LGKDQQEAGVQNVTVKTVTFTGTENGVRIKSWGRPSTGFARSILFQHIVMTNVQNPIVID
                                                                                                                                                                                                                                                                                         NASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKNSNVPF
                                       SGKPSEATCKNVHFNNAEHVTP 440
                                                                                QNYCPNDKGCPGQASGVKVSDVTYQDIHGTSATEVAVKFDCSSMYPCNGIRLQDVKLT-Y 372
                                                                                                                        QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE 418
                                                                                                                                                                                                          LGSGNSEAYVSNVTVNEAKIIGAENGVRIKTW-QGGSGQASNIKFLNVEMQDVKYPIIID 358
                                                                                                                                                                                                                                                    NAAGNSPNTDGIHVQMSSGVTILDSKISTGDDCVSVGPGTTNLWIENVACGPGHGISIGS
                                                                                                                                                                                                                                                                                                                                     GLW--DCK-SSGKSCPSGATTLSFSNSNNVVVSGLISLNSOMFHIVVNGCQNVKMQGVKV 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 398;
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; Sequence 284649, Application US/10424599

RESULT 14 US-10-424-599-284649

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RESULT 15
US-10-437-963-155040
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Caho Yihua
APPLICANT: Caho Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules ITITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 284649
                                                                                                                                                                                                                                                                                                  Sequence 155040, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 155040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 155;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                     APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No. US20040031072A1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             453 DDPFCWNAYGTQETLTIPPINCLREGDPETV 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96
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                                                                                                                                                                                                        Zhou, III...
                                                                                                                                                                                                                               Kovalic, Dav.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEATCKNVHFNNAEHVTPHCTSLEISEDEAL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KE-CLNOTSAVHVNDVSYSNIKGTYDVRTAPIHFACSDTVACTNITLSEVELLPFEGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEPCIQQESAVQVKNVVYENIKGTSATKVA-IKFDCSTNFPCEGIIMENINLVG-ESGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPNTDGIHVENSKYVGIYNSMISNGDDCISIGPGSSNVDIAGLTCGPSHGISIGSLGVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFQVDGTLMAPDGPNSWPEADSRNQWLVFYRLDQMTLNGTGTIEGNGDKWWDLPCKPHRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVKIFGSLEASSKISDYKD----RRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINK- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQACVSNLTVRDSIIRESDNGLRIKTWQGGMGSVSSLRFENIQMENVGNCIIIDQYYCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDR
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                                                                                                                                                                                                   Cao, You
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGN
                                                                                                                                                           Barbazuk, Brad
                                                                                                                                                                          Boukharov, Andrey A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 40
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT4530_54842C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
 377
                                                             317
                                                                                            363
                              421
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                                                                                                                                                          310
                                                                                                                                                                                       201
                                                                                                                                                                                                              250 GVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYV
                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                               190 KSLECRDAPTALTEWNCKNLKVNNLKSKNAQQIHIKEESCINVVASNLMINASAKSENID 249
                                                                                                                                                                                                                                                                                                                                              132 SS-ISVKIFGSLEA-SSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKIN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                           148;
                                                                                                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                         72 GIKVINVLSFGAKGDGKTYDNIAFEQAMNEACSSRTPVQFVVPKNKNYLLKQITFSGPCR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400
                                                                                                                                                                                                                                                                                                               GGRMIVQIDGTLVAPSGYTGSASSGGEWIVFDHVDGLTV-SGGTLDGRGESLW--ACKAA
                                                                                                                                              SNYTVNEAKIIGAENGVRIKTWQGGSGQAS-----NIKFLNVEMQDVKYPIIIDQNYC
                                                                                                                                                                                       GIHVQSSSAVTITGASIQTGDDCISVGPGTSNLRVEHVSCGPGHGISIGSLGKESEEGGV
                                                                                                                                                                                                                                                   GHGGCPDGATSMKVLNSRDVVISGVKSVNSELYHVVIDGCEGVAVQDARIVAPGSSPNTD
                              KPSEATCKN 429
                                                            PNDGGQGCPHQSSDVQISGVTYTDIQGSSASQVAVKFDCSASKPCSGLGLQDIKLTFDGG
                                                                                 --DRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESG
                                                                                                                                                                                                                                                                                                                                                                             GAAVYNVESYDARPDGRTDASRALASAWSAACRSPEPATVYVPDGE-FFVSHSAFAGPCS
KPAEATCQH
                                                                                                                           ENVIVSGAAFVGTENGLRIKTW----GRAARSGAYVRGVVFEHALMRDVSNPIIIDQSYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 701.5; DB 1
Pred. No. 3.9e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                       133;
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Job time : Search completed: July 21, 2004, 17:17:48 82.2655 secs

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Minimum DB seq length: 0
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2390
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Listing first 45 summaries
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            pir2:*
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1497.381 Million cell upda
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	29	28	27	26	20	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	o,	υī	4	w	2	1	No.	Result
	702.5	704	704	704.5	708.5	710.5	711.5	715	718	718.5	727	728	736	741.5	749.5	764	787	787.5	787.5	796.5	840.5	898.5	1091	1108	1115.5	1127	1128	1142	2390	Score	
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	394	374	374	387	422	365	387	392	435	395	392	405	423	491	1161	507	514	514	434	514	468	459	460	458	426	431	461	462	457	Length	
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	G86190	T04672	B85421	T04322	S34199	T04319	T04320	T00669	T48638	T05906	S57806	D84871	T08213	B86155	B86368	JC7366	JC2498	S48730	A96609	JC7100	H96728	D96833	T17011	S71523	H84846	T46187	T08215	S31195	A25534	ij	
1	hynothetical prote	polygalacturonase	probable polygalac	polygalacturonase	polygalacturonase	polygalacturonase	polygalacturonase	probable polygalac	polygalacturonase-	probable polygalac		probable polygalac	polygalacturonase	probable polygalac	ein	Jun a 2 protein -	<u>π</u>	Cry j II protein -	probable polygalac	polygalacturonase	probable polygalac	hypothetical prote	polygalacturonase	polygalacturonase	probable polygalac	polygalacturonase	polygalacturonase	polygalacturonase	lacturonase	Description	

A;Molecule type: mRNA
A;Residues: 1-457 <SHE's
A;Residues: 1-457 <SHE's
A;Residues: 1-457 <SHE's
A;Cross-references: EMBL:X05656; NID:g19297; PIDN:CAA29148.1; PID:g19298
A;Note: part of this sequence, including the amino end of the mature protein, was confix
R;Nose, R.E.; Houck, C.M.; Monson, E.K.; DeJesus, C.E.; Sheehy, R.E.; Hiatt, W.R.
Nucleic Acids Res. 16, 7191, 1988
Nucleic Acids Res. 16, 7191, 1988
A;Title: The nucleotide sequence of the 5' flanking region of a tomato polygalacturonase
A;Reference number: S02101; MUID:88303350; PMID:3405769

A; Reference number: S06340 A; Accession: S06340

A;Molecule type: DNA
A;Residues: 1-457 <BIR>
A;Residues: 1-457 <BIR>
A;Cross-references: EMBL:X14074; NID:g19305; PIDN:CAA32235.1; PID:g295813
C;Comment: The polygalacturonase, a single cell wall enzyme, is the major
C;Superfamily: polygalacturonase
C;Keywords: g1ycosidase; hydrolase; polysaccharide degradation

major enzyme mediatı

Plant Mol. Biol. 11, 651-662, 1988 A;Title: The tomato polygalacturonase gene and ripening-specific expression in transgen: A;Reference number: S08504 A;Accession: S08504

A;Cross-references: EMBL:X07410; NID:g19295; PIDN:CAA30308.1; PID:g19296 R;Bird, C.R.; Smith, C.J.S.; Ray, J.A.; Moureau, P.; Bevan, M.W.; Bird, J.Plant Mol. Biol. 11, 651-662, 1988

A.S.; Hughes,

A;Accession: S02101 A;Molecule type: DNA A;Residues: 1-93 <ROS>

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
659	662.5	667	673	673.5	678.5	680.5	683	684	687	687.5	688.5	690	696	698.5	701.5
27.6	27.7	27.9	28.2	28.2	28.4	28.5	28.6	28.6	28.7	28.8	28.8	28.9	29.1	29.2	29.4
414	664	407	444	387	445	394	394	397	383	393	492	540	384	452	542
N	N	2	N	N	N	N	N	N	N	2	2	N	2	N	N
E85204	A84742	S52006	S34200	T07591	S34266	T00668	F86190	F96680	T47809	S40123	C96521	B96631	E84871	C85024	нв6239
polygalacturonase-	probable polygalac	polygalacturonase	polygalacturonase	polygalacturonase	polygalacturonase	probable polygalac	hypothetical prote	F5I14.10 [imported	polygalacturonase-	polygalacturonase	protein F21D18.18	probable polygalac	probable polygalac	probable polygalac	protein F20B24.8 [

# ALIGNMENTS

# RESULT 1 A25534 A25534 polygalacturonase (EC 3.2.1.15) precursor - tomato NyAlternate names: pectinase; poly[1,4-alpha-d-galacturonide]glucanohydrolase C;Species: Lycopersicon esculentum (tomato) C;Date: 30-Jun.1988 #sequence revision 30-Jun.1988 #text\_change 22-Jun-1999 C;Accession: A25534; JA0156; S06340; S02101; S08504 R;Grierson, D.; Tucker, G.A.; Keen, J.; Ray, J.; Bird, C.R.; Schuch, W. Nucleic Acids Res. 14, 8595-8603, 1986 A;Title: Sequencing and identification of a cDNA clone for tomato polygalacturonase. A;Reference number: A25534 A;Accession: A25534 A;Accession: A25534 A;Residues: 1-457 <GRI>A;Accession: A25534; MUID:87066731; PMID:3786135 A;Cross-references: GB:X04583; NID:g19291; PIDN:CAA28254.1; PID:g19292 R;DellaPenna, D.; Bennett, A.B. Plant physiol. 86, 1057-1063, 1988 A;Title: In vitro synthesis and processing of tomato fruit polygalacturonase. A;Accession: JA0156 A;Access

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RESULT 2
S31195
S31195
CJSpecies: Persea americana (avocado)
CJSpecies: Persea americana (avocado)
CJSpecies: Persea americana (avocado)
CJSpecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CJAccession: S31195; S28072
RJDOPICO, B.; Lowe, A.L.; Wilson, I.D.; Merodio, C.; Grierson, D.
RJTHIC: Cloning and characterization of avocado fruit mRNAs and their expression: A; Merece number: S31195; MUID:93184201; PMID:8095163
A;Accession: S31195
A;Accession: S31195
A;Rocession: S31195

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A;Reference number: $28072
A;Accession: $28072
A;Molecule type: mRNA
A;Residues: 1-81'5',183-462 <DO2>
A;Residues: 1-81'5',183-462 <DO2>
A;Cross-references: EMBL:X66426; NID:g22630; PIDN:CAA47055.1; PID:g22631
C;Superfamily: polygalacturonase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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Pred. No. 2.6e-73;
7; Mismatches 106;
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A; Residues: 1-461 < HAI
A; Cross-references: El
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A;Accession: T08215
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                            302
                                                                                                                                                                                                                                                                                   133 PITFSGPCNSPLLFQIEGTVKASPHISDYEKDRRHWIIFQNLLGLRVEGKGIINGNGRKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 TFLFVVVVNFDTFSTCFGSYPDVDNPLPSISSGDKEDYGQHYYEHSSSEFSSMLRT--RL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
SGNSEAYVSNYTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNYEMQDVKYYPIIIDQNY
                                                                                                                                                                                                                                                                                                                                                                                                                             DKVDKNGI----KVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILLLIIIFASSISTCRSNVID-DNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTI
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                                                                                                                     SAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLG 301
                                                                                                                                                                                                                                 WPSSCKINKSLPCRDAPTALITEWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
                                                                                                                                                                                                                                                                                                                                                                                      EKMVSSPLASPEIFNVDDYGAMGDGED-DTEAFKETWKDACSSTNAI-FLVPCDRVYHLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGTSASEVAVKFDCSKSSPCQGYIVGNINLVGNGGKETTMSCSNI
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                                                                              PGNSPNTDGIHVTGTQFIVIKNCLIMTGDDCISIVSGSKNVRAKGITCGPGHGISIGSLG
                                                                                                                                                                                  WINSCKVNKTLPCKEAPTAVTFYQCTNLRVEGLRFRNAQQMLLSFQRCNNVKALNLWIYA
                                                                                                                                                                                                                                                                                                                                  QITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGGGTINGNGQVW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGTGDDCISIESGSKMVIATNITCGPGHGISIGSLGDRNSEAHVSGVLVDGGNLFDTTNG
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Pred. No. 2.5e-72;
9; Mismatches 129;
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A;Reference number: Z23014
A;Reference number: Z23014
A;Recession: T46187
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-431 <BEN>
A;Residues: 1-431 <BEN>
A;Cross-references: EMBL:AL133248; PIDN:CAB66108.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: Dehiscence-related expression of an Arabidopsis thaliana A;Reference number: Z25172
A;Accession: T50674
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-431 <JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polygalacturonase (EC 3.2.1.15) precursor [similarity] - N;Alternate names: protein T8H10.110 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_C;Accession: T46187; T50674 R;Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Mewe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 3
A;Introns: 85/3; 129/3; 186/3; 193/3; 263/1; 290/2; 326/3; 364/3
C;Superfamily: polygalacturonase
C;Keywords: glycosidase; hydrolase
C;Keywords: glycosidase; hydrolase
F;1-27/Domain: signal sequence #status predicted <SIG>F;28-431/Product: polygalacturonase #status predicted <MAT>
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R;Jenkins, E.S.; Roberts, J.A.
submitted to the EMBL Data Library, December 1997
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T46187
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A;Experimental source: cultivar Landsberg erecta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Mewo
submitted to the Protein Sequence Database, January 2000
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Matches 223
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GISIGSLGSGNSEAYVSNUTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKY
                                                                                                                                                                                    INGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
                                                                                                                                                                                                                                             DDKSAQAEASCKNVKWKNRGRVSPQC
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                                                                                VSNVEITÄPGDSPNTDGIHITNTQNIRVSNSDIGTGDDCISIEDGTQNLQIFDLTCGPGH
                                                                                                       ASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGH
                                                                                                                                                                                                                                                                                     NKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GT
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                                                                                                                                                              INGNGKTWWQNSCKIDKSKPCTKAPTALTLYNLKNLNVKNLRVKNAQQIQISIEKCNKVE
                                                                                                                                                                                                                                                                                                                                                                   SKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPK
                                                                                                                                                                                                                                                                                                                                                                                                              AVFLCVLLMLSLCKALSSNVDDGYGHEDGSFESDSLLKLNNDDVL-----SLISSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.2%; Score 1127; DB 2;
49.6%; Pred. No. 2.7e-72;
ative 71; Mismatches 116;
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                                                                                                                                                                                                                                                                                                                             ----TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLVPK
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A;Gene: At2g41850
A;Map position: 2
C;Superfamily: po
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84846
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable polygalacturonase [imported] - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_charc;Accession: H84846
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIIIDQDYCDK-DKCEDQESAVQVKNVVYKNISGTSATDVAITLNCSEKYPCQGIVLENV
                                                                                                              QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE 418
                                                                                                                                                           SLGDDNSKAFVSGVTVDGAKLSGTDNGVRIKTYQGGSGTASNIIFQNIQMDNVKNPIIID
                                                                                                                                                                                              SLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIID
                                                                                                                                                                                                                                      VTAPADSPNTDGIHITNTQNIRVSESIIGTGDDCISIESGSQNVQINDITCGPGHGISIG
                                                                                                                                                                                                                                                                             INASAKSPNTDGVHVSNTQXIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIG
                                                                                                                                                                                                                                                                                                                       ETWWQNSCKRNKA---
                                                                                                                                                                                                                                                                                                                                                            QVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLM
                                                                                                                                                                                                                                                                                                                                                                                                    LKSIQLTGPCNSILTVQIFGTLSASQKRSDYKDISKWIMFDGVNNLSVDGGDTGVVDGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                     LKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GTINGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLVTVFLLWALLMESWCKASRISPNVYDHSYKRFKSDSLIKRR--EDITGLRSFVRASLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIKG---
                                     SGKPSEATCKNVHFNNAEHVTPHCTS
                                                                            QDYCDK-SKCTTEKSAVQVKNVVYRDISGTSASENAITFNCSKNYPCQGIVLDRVNIKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
-GKATCTNANVVDKGAVLPQCNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE002093; NID:g2335094; PIDN:AAC02763.1;
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49.8%;
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Pred. No. 1.7e-71;
4; Mismatches 117;
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RESULT S71523

polygalacturonase
N;Alternate names:

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[similarity]

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S71525
A;Molecule type: DNA
A;Residues: 265-458 <LEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X77231
A;Experimental source: cultivar Maravilla
A;Experimental source: revised in reference
A;Note: this sequence has been revised in reference
R;Lester, D.R.; Speirs, J.; Orr, G.; Brady, C.J.
Plant Cell Env. 13, 513-521, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: this is a revision to the sequence from reference 8715 R;Lester, D.R.; Speirs, J.; Orr, G.; Brady, C.J. submitted to the EMBL Data Library, January 1994 A;Description: Homologies to the tomato endopolygalacturonase A;Reference number: $71524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lee, E., Speirs, J.; Gray, J.; Brady, C.J.
submitted to the EMBL Data Library, April 1994
A;Description: Homologies to the tomato endopolygalacturonase
A;Reference number: S71523
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A;Experimental source: cultivar Maravilla
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Best Local S
Matches 226
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Residues: 53-92,'I',94-149,'T',151-185,'W',187-196,'THA',200,'ESLS',206-207,'TNT',212
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Date: 19-Mar-1997 #sequence revision 19-Mar-1997

Accession: $71523; $71524; $71525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVIQRNSILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLS----
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                                      NFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHCT
                                                                                                     FLNVEMQDVKYPIIIDQNYCD-RVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCST
                                                                                                                                                                                                                                                                                                                                                                                                                                            SSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSV
                                                                                                                                                               QATDITCGPGHGISIGSLGEDNANDHVSGVFVNGAKISGTSNGVRIKTWQGGSGSASNIV
                                                                                                                                                                                                     QATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIK
                                                                                                                                                                                                                                               HVRFQNCKNVEASHLTVTAPEDSPNTDGIHITNTKNITISSSVIGTGDDCISIVSGSQRV
                                                                                                                                                                                                                                                                                    HIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNV
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                                                                                                                                                                                                                                                                                                                          QSLLVVGPGTINGNGNRWWENSCKRKPQPPCNEQAPTAVTFNKCNNLVVKNLKIQDAQQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolase; polysaccharide degradation
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48.9%; Pred. No. 6.
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-QNARAKCNNVKPAYKGAVSPRCS
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C;Accession: D96833
R;Theologis, A.; Ecker, J.R.; Palm, C.
Chin, C.W.; Chung, M.K.; Conn, L.; Cc
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu,

C.J.; Federspiel, N.A.; Kaul, S.; White, (Conway, A.B.; Conway, A.R.; Creasy, T.H.;

0.;

Dewar, Alonso, ewar, K.; #text\_change 23-Mar-2001

, J.; Liu,

Johnson-Hopson, C.; Khan, S.; S.X.; Liu, Z.A.; Luros, J.S.;

Khaykin, E.; Maiti, R.; Ma

Marziali,

RESULT D96833

hypothetical protein F18B13.25 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change

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polygalacturonase (EC 3.2.1.15) - apple tree N;Alternate names: poly [1,4-a.D-galacturonide] glycan hydrolase C;Species: Malus domestica (apple tree) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change : C;Accession: T17011
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C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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A;Experimental source: strain Golden delicious; ripe fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: A cDNA clone for endopolygalacturonase from apple A;Reference number: Z18649; MUID:95062722; PMID:7972500 A;Accession: T17011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRR 155
AITLNCSQSVPCQGIVLQSVQL--QNGR---AECNNVQPAYKGVVSPRC 460
                           AIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHC 442
                                                                                                                                                                                                                                IVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGG 334
                                                                                                                                                                                                                                                                                        NIQDAQQIHVIFQNCINVQASCLTVTAPEDSPNTDGIHVTNTQNITISSSVIGTGDDCIS
                                                                                                                                                                                                                                                                                                                                   KSKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCIS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                   LWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLPCRD-APTALTFWNCKNLKVNNL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKAWKAACSSSGAMVLVVPQ-KNYLVRPIEFSGPCKSQLTLQIYGTIEASEDRSIYKDID 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIEGLKVMELIRPRTQLFSSRKLNTI-TGGIATSSAPAKTISVDDFGAKGNGAD-DTQAF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MALKTQLLWSFVVVFVVSFSTTSCSGSSFQEVNALHSYVDHVDDKESGYNSRAYPSY-TD 59
                                                                                        SGSATNIVFONVOMNDVTNPIIIDONYCDHKTKDCKQQKSAVQVKNVLYQNIRGTSASGD 416
                                                                                                                                     SGQASNIKFLNVEMQDVKYPIIIDQNYCD-RVEPCIQQFSAVQVKNVVYENIKGTSATKV 393
                                                                                                                                                                                        IVSGSQRVQATDITCGPGHGISIGSLGEDGSEDHVSGVFVNGAKLSGTSNGLRIKTWKGG
                                                                                                                                                                                                                                                                                                                                                                                      HWLIFDNVQNLLVVGPGTINGNGNIWWKNSCKIKPQPPCGTYAPTAVTFNRCNNLVVKNL
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49.3%; Pred. No. 1.1e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNNNIDKVDKNGI-----KVINVLSFGAKGDGKTYDNIAF
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D9683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-459 <53TO>
A;Cross-references: GB:AE005173; NID:g5902387; PIDN:AAD55489.1; GSpnp-C.;GenetLos:
A;GenetLos:
A;GenetLo
probable polygalacturonase F24J13.7 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Cpate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-20 C;Accession: H96728 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Whi Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Creasy, T ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khayk C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Su ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Rocession: H96728 A;Roteaus: preliminary A;Molecule type: DNA A;Residues: 1-468 <8T0>
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Best Local S
Matches 188
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Pred. No. 4.6e-56;
2; Mismatches 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
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                                                                                                                                                                                                                                                                                                               Khaykin, E.; Kim, C
Maiti, R.; Marziali
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polygalacturonase Cha o 2 - Japanese cypress
C;Species: Chamaccypris obtusa (Japanese cypress)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_chamaccypris obtusa (Japanese cypress)
C;Accession: JC7100; PC7026
R;Mori, T: Yokoyama, M.; Komiyama, N.; Okano, M.; Kino, K.
Biochem. Biophys. Res. Commun. 263, 166-171, 1999
A;Titla: Purification, identification, and cDNA cloning of (A;Reference number: JC7100; MUID:99417540; PMID:10486272
A;Accession: JC7100
A;Molocule type: mRNA
A;Residues: 1-514 <MOR>
A;Accession: PC7026
A;Accession: PC7026
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C;Genetics:
A;Gene: F24J13.7
A;Map position: 1
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TFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPS
                                                                                                                                                ILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNIDK 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIVNGSAKIKMKRIYCGPGHGISIGSLGQGHSKGTVTAVVLETAFLKNTTNGLRIKTWQG
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                                                LVHSRHDAATVFNVEQYGAVGDGKHDSTEAFATTWNAACKKASAV-LLVPANKKFFVNNL
                                                                              V---DKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTFVQFVVPKNKNYLLKQI
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41.6%;
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Pred.
                                                                                                                                                                                 Score 796.5; DB Pred. No. 9e-49; 3; Mismatches 16
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Who Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;fittle: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
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A;Map position: 1
C;Superfamily: po
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C;Genetics:
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A;Accession: A96609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable polygalacturonase F25P12.85 [imported] - Arabidopsis thaliana (cypecies: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
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Best Local Similarity
Matches 170; Conserv
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Superfamily:
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                                                                                                                                                                                                                                                                                                         112 VVPKNKNYLLKQITFSGPCRSSISVKIFGSLEA----SSKISDYKDRRLWIAFDSVQNLV
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                               NVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSQQASN
                                                                                                                                    QIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQ
                                                                                                                                                                                                                                                                   LVPYTFCFLVKPTTFNGPCRTNLVLQIDGFIVSPDGPRSWPSNY--QRQWMFYRVNGLS
                                                                                                                                                                                                                                                                                                                                                                                            YLSKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTP--VQF
                                                                                           QFHVRFDNCSDVVVDSVIIKAPASSPNTDGIHIENTHNVQIRNSMISNGDDCISIGAGCF
                                                                                                                                                                              IQGSGVINGRGQKWWNLPCKPHKGLNGTTQTGPC-DSPVAIRLFQSSKVRIQGINFWNSA
                                                                                                                                                                                                                                                                                                                                                      YLSPSPAPNPAYNDNDNIAPTVFDVTSFGAIGDCSTDDTSAFKMAWDAACMSTGPKSALL
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        NVDIKNVTCGPSHGISIGSLGVHNSQAYVSNITVTNSTIWNSDNGVRIKTWQGGSGSVSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 787.5; DB 2;
Pred. No. 3.1e-48;
8; Mismatches 155;
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Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Southwick, A.M.; Sun,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 434;
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second major allergen Cry j II precursor - Japanese cedar (,Species: Cryptomeria japonica (Japanese cedar) C,Species: Cryptomeria japonica (Japanese cedar) C;Date: 16-Mar-1995 #sequence revision 26-May-1995 #text_change C,Accession: JC2498; PC2346, Ā60147 R;Komiyama, N.; Sone, T.; Shimizu, K.; Morikubo, K.; Kino, K. Biochem. Biophys. Res. Commun. 201, 1021-1028, 1994 A;Title: CDNA cloning and expression of Cry j II, the second ma,Reference number: JC2498; MUID:94271186; PMID:8002972
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RESULT 12
$48730
Cry j II protein - Japanese cedar
Cry j II protein - Japanese cedar
Cry j II protein - Japanese cedar
Cry j II protein - Japanese cedar
CrySpecies: Cryptomeria japonica (Japanese cedar)
CryDate: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
CryDate: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
CryDate: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
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A;Residues: 1-514 <NAM>
A;Cross-references: GB:D37765; NID:g577695; PIDN:BAA07021.1; PID:d1007598; PID:g577696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 353, 124-128, 1994
A; Title: Molecular cloning of the second major allergen,
A; Reference number: S48730; MUID:95010777; PMID:7926035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        뮍
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-- IASCINDNANGYFSGHVIPACKNISPS
                                                                                                                                                                                                                                                                                                             SGNSEAYYSNYTYNEAKIIGAENGYRIKTWQGGSGQASNIKFLNYEMQDYKYPIIIDQNY 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCK-INKSLPC--RDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
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                                                            PSEATCKNVHFNN--AEHVTPHCTSLEIS 448
                                                                                                                                                                                                 CDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESGK 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VD---KNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQI 124
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                                                                                                                                 CTSASACQNORSAVOIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSGK
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; Pred. No. 3.9e-48;
78; Mismatches 163;
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433
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Kur ס

the second major allergen

of Japanese

21-Jul-2000

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Biochem. Biophys. Res. Commun. 275, 195-;
A;Title: Purification, identification, and A;Reference number: JC7366
A;Accession: JC7366
A;Molecule type: mRNA
A;Residues: 1-507 <YOK-
A;Cross-references: GB:AJ404653
A;Accession: PC7093
A;Molecule type: protein
A;Residues: 55-63 <YO2-
C;Comment: This protein, a second major of the polygalacturonase family.
C;Keywords: glycoprotein; pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Sakaguchi, M.; Inouye, S.; Taniai, M.; Ando, S.; Usui
Allergy 45, 309-312, 1990
A;Title: Identification of the second major allergen of
A;Reference number: A60147; MUID:90342988; PMID:2382797
A;Accession: A60147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: glycoprotein; pollen F;1-54/Domain: signal sequence #status predicted F;55-460/Product: second major allergen Cry j #st F;429,460,472/Binding site: carbohydrate (Asn) (c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: JC2498
A;Molecule type: mRNA
A;Residues: 1-514 <KOM>
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                                                                                                                                                                                                                                                            C;Species: Juniperus ashei (mountain cedar)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change
C;Accession: JC7366; PC7093
R;Yokoyama, M.; Miyahara, M.; Shimizu, K.; Kino, K.; Tsunoo, H.
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Best Local Similarity
Matches 168; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNN--AEHVTPHCTSLEIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGSSNIVIEDL1CGPGHGISIGSLGRENSRAEVSYVHVNGAKFIDTQNGLRIKTWQGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt LMNSPEFHLVFGNCEGVKIIGISITAPRDSPNTDGIDIFASKNFHLQKNTIGTGDDCVAII}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFDSVQNLVVGGGGTINGNGQVWWPSSCK-INKSLPC--RDAPTALTFWNCKNLKVNNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WQAACKNPS-AMLLVPGSKKFVVNNLFFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WNEACSSRIPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AHDFQAYL---SYLSKNIESNNNIDKVD---KNGIKVINVLSFGAKGDGKTYDNIAFEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMASHIIYENVEMINSENPILINQFYCTSASACQNQRSAVQIQDVTYKNIRGTSATAAAI
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Pred. No. 4.2e-48;
                                           major allergen
                                                                                                                                                                                                                  zu, ...
195-202, zu, and cDNA
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wunder, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: B86368
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
C;Accession: B86368
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A;Gene: F28C11.9
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A; Residues: 1-1161 <STO>
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IAPDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSK: | :: : | | | | | : | | | | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                              73;
                                                                                                                                                                                                                                                                                                                                                                                           Score 749.5; DB 2;
Pred. No. 5.8e-45;
3; Mismatches 133;
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Pred. No. 1.8e-46;
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Maiti, R.; M
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galactosiduronic linkages in pectate and other galacturonans:- SUBCELLULAR LOCATION: Secreted:- SUBCELLULAR LOCATION: Secreted:- BIOTECHNOLOGY: The effect of FG can be neutralized by introducing an antisense PG gene by genetic manipulation. The Flavr Savr tomato produced by Calgene (Monsanto) in such a manner has a longer shelf life due to delayed ripening:- SIMILARITY: Belongs to family 28 of glycosyl hydrolases	DENCE FROM N.A.  Leby R.E., Pearson J., Brady C.J., Hiatt W.R.;  lechy R.E., Pearson J., Brady C.J., Hiatt W.R.;  lechiar characterization of tomato fruit polygal  lechiar denaracterization of tomato fruit polygal  TISIONS.  IT W.R.;  FUNCTION: Acts in concert with the pectinesters  process. Is involved in cell wall metabolism, s  polyuronide degradation.  PONTIVET ACTITUTY. Bandom bydrolysis of 1.4-al	SEQUENCE FROM N.A. STRAIN=cv. Ailsa Craig; Bird C.R., Smith C.J.S., Ray J.A., Moureau P., Bevan M.W., Bird A.S., Hughes S., Morris P.C., Grierson D., Schuch W.; "The tomato polygalacturonase gene and ripening-specific expression in transgenic plants."; plant Mol. Biol. 11:651-662(1988).  [2] [2] [3] [2] [3] [4] [5] [5] [6] [7] [8] [8] [8] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9	LT 1  _IXCESIXCES STANDARD; PRT; 457 AA.  PGIR LYCES STANDARD; PRT; 457 AA.  POSII7;  13-AUG-1987 (Rel. 05, Created)  13-AUG-1987 (Rel. 05, Last sequence update)  10-OCT-2003 (Rel. 42, Last annotation update)  Polygalacturonase 2A precursor (EC 3.2.1.15) (PG-2A) (Pectinase).  Lycopersicon esculentum (Tomato).  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; asterids;  NCBI TaxID=4081;  [1]TaxID=4081;

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an email to license@isb-sib.ch).
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ACT_SITE
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A polygalacturonase gene from kiwifruit (Actinidia deliciosa).";
Plant Physiol. 103:669-670(1993).
-!- FUNCTION: Acts in concert with the pectinesterase, in the ripe process. Is involved in cell wall metabolism, specifically in polyuronide degradation.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRO00743; Glyco_hydro_28.
Pfam; PF00295; Glyco_hydro_28; 1.
PROSITE; PS00502; POLYGALACTURONASE;
Hydrolase; Glycosidase; Cell wall; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + +
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MEDLINE=94302157; PubMed=8029342;
Atkinson R.G., Gardner R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Ericales; Actinidiaceae; Actinidia.
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SUBCELLULAR LOCATION: Secreted.
DEVELOPMENTAL STAGE: In ripening
SIMILARITY: Belongs to family 28
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TNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHCTSLEISEDE
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POLYGALACTURONASE.

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Pred. No. 1.1e
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l.1e-83;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Ripening-related polygalacturonase cDNA from avocado."
Plant Physiol. 103:289-290(1993).
-!- FUNCTION: Acts in concert with the pectinesterase,
process. Is involved in cell wall metabolism, speci
polyuronide degradation.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-
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STRAIN=cv. Hass; TISSUE=Pericarp;
MEDLINE=93184201; PubMed=8095163;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     galactosiduronic linkages in pectate and other galacturo-
:- SUBCELLULAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: In ripening fruit.
-!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dopico B., Lowe A.L., Wilson I.D., Merodio C., Grierson D.; "Cloning and characterization of avocado fruit mRNAs and their expression during ripening and low-temperature storage."; Plant Mol. Biol. 21:437-449(1993).
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Ol-JUL-1993 (Rel. 26, Last sequence update)
10-JCT-2003 (Rel. 42, Last annotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG)
                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L06094; AAA32914.1; PIR; S31195; S31195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                  SIGNAL
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InterPro; IPR006626; PbH1.
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; SM00710; PbH1; 5.
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POLYGALACTURONASE; 1.
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                                            Score 1136;
                                                                                                                                                                                                                                    POLYGALACTURONASE.
BY SIMILARITY.
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  d. No. 1.7
                                                                                                                   REF.
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                                            Length 462;
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RESULT 4
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"A cDNA clone for endopolygalacturonase from apple.";

"A cDNA clone for endopolygalacturonase from apple.";

Plant Physiol. 105:1437-1438(1994).

-!- FUNCTION: Acts in concert with the pectinesterase,

process. Is involved in cell wall metabolism, speci-
polyuronide degradation.

-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996
01-FEB-1996
10-OCT-2003
                             EMBL; 127743; AAA74452.1; -.

PIR; T17011; T17011.

InterPro; IPR000743; Glyco_hydro_28.

Pfam; PF00295; Glyco_hydro_28; 1.

PROSITE; PS00502; POLYGALACTURONASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRUIN-CV. Golden Delicious;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
Malus domestica (Apple) (Walus sylvestris).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; coeurosids I; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P48978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGLR_MALDO
             Hydrolase;
                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95062722; PubMed=7972500;
                                                                                                                                                                                                                                                                                                                galactosiduronic linkages in posus SUBCELLULAR LOCATION: Secreted
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               Glycosidase; Cell wall; Signal;
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Best Local
                                                                                                                                                                                                                                                                                                                                                           CHAIN
ACT SITE
CARBOHYD
CARBOHYD
                      MEDLINE=94271186; PubMed=8002972;
Komiyama N., Sone T., Shimizu K., Mc
"cDNA cloning and expression of Cry
Japanese cedar pollen.";
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                    Japanese cedar pollen.";
FEBS Lett. 353:124-128(1994)
                                                                                                                                                                                           Namba M., Kurose M., Torigoe K.,
Usui M., Kurimoto M.,
"Molecular cloning of the second
                                                                                                                                                                                                                                                              MEDLINE=95010777; PubMed=7926035;
                                                                                                                                                                                                                                                                                TISSUE=Pollen;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
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                                                                                       SSUE=Pollen;
                                                                                                                                                                                                                                                                                                                                                    TaxID=3369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRYJA
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POLYGALACTURONASE.

PROBABLE.

PROBABLE. (GLCNAC. . .) (POTENTIAL CALCINAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1091; DB 1;
Pred. No. 2.4e-69;
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                                                                                                                                                                                               major allergen,
                                                                                                                                                                                                                                     Hino K.,
                                          Morikubo K.,
                      j II the
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                                                                                                                                                                                                                                     Taniguchi Y., Fukuda S.,
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                        allergen
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                        of.
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EMBL; D29772; BAA06172.1; -
PIR; JC2498; JC2498.
PIR; S48730; S48730.
HSSP; P26509; 1BHE.
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InterPro; IPR006626; PbH1.
Pfam; PF00295; Glyco hydro 28; 1.
SMART; SM00710; PbH1; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pollen.";
Allergy 45:309-312(1990).
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amyloplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00502; POLYGALACTURONASE; Hydrolase; Glycosidase; Cell wall; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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Sakaguchi M., Inouye S., Taniai M., Ando S.,
"Identification of the second major allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 201:1021-1028(1994)
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                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                swiss-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation-
European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactosiduronic linkages in pectate and other galacturonans. SUBCELLULAR LOCATION: SECRETED OR AMYLOPLAST (POTENTIAL). ALLERGEN: Causes an allergic reaction in human. SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
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                                                                                                                                                                                                              Similarity
                                              FINGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTLMGKGVIDGQGKQWWAG
                                                                                                                                                              ILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNIDK 67
QCKWVNGREICNDRDRPTAIKFDFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITA
                       SCK-INKSLPC--RDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
                                                                    TESGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPS 184
                                                                                                                      VD---KNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQI 124
                                                                                                                                                VAMQLIIMAAA-----EDQSAQIMLDSDIEQ-----YL----RSNRSLRK
                                                                                                VEHSRHDAINIFNVEKYGAVGDGKHDCTEAFSTAWQAAC-KKPSAMLLVPGNKKFVVNNL
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514 PA;
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                                                                                                                                                                                                                                                  56645 MW;
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                                                                                                                                                                                                                                              DI -> VV (IN REF. 2).
Q -> K (IN REF. 2).
K -> N (IN REF. 2).
N -> S (IN REF. 2).
N -> S (IN REF. 2).
X -> E (IN REF. 2).
X -> I (IN REF. 2).
M -> I (IN REF. 2).
M -> C (IN REF. 2).
R -> C (IN REF. 2).
R -> C (IN REF. 2).
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N-LINKED
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F -> L (IN REF.
V -> L (IN REF.
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ع کی ۔
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of Japanese
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AN White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

AN Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

AN Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

AN Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

AN Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

AN Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

AN Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

AN Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

AN LIN X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

AN Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

AN Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Renase clone GBGEB184 precursor (EC 3.2 (Pectinase) (Galacturan 1,4-alpha-galacturonidase).
PGA3 OR ATIGO2790 OR T14P4_2 OR F22D16.22.
Arabidopsis thaliana (Mouse-ear cress).
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P49062;
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                                                                                Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Differential expression of a polygalacturonase Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99413295; PubMed=10485285; Torki M., Mandaron P., Thomas F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21016719; PubMed=11130712;
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STRAIN=CV. C24;
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                                  polygalacturonase.
CATALYTIC ACTIVITY
                                                                   development,
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                LYTIC ACTIVITY: \{(1,4)-alpha-D-galacturonide\}(N)
4)-alpha-D-galacturonide\}(N-1) + D-galacturonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Columbia;
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                                                                   germination,
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                                                                   in depolymerizing p
on, and tube growth.
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Best Local Similarity
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P48979;
01-FEB-1996
01-FEB-1996
10-OCT-2003
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ACT SITE
CARBOHYD
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CARBOHYD
SEQUENCE
                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG)
Prunus persica (Peach).
Eukaryota; Viridiplantae; Streptophyta; Embryo)
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SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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InterPro; IPR006626; PbH1.
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Y16230; CAA76127.1; -.
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Streptophyta; Embryophyta;
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Pred. No. 1.
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                     Tracheophyta;
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Spermatophyta;

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-i- FUNCTION: Acts in concert with the pectinesterase, in the process. Is involved in cell wall metabolism, specifically polyuronide degradation.

-i- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonic SUBCELLULAR LOCATION: Secreted.

-i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X76735; CAA541; PIR; S40123; S40123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some send an email to license@isb-sib.ch).
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"Peach (Prunus persica) endopolygalacturonase cDNA isolation and mRNA
analysis in melting and nonmelting peach cultivars.";

Diagraphysical for control of the peach cultivars."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P26509;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00295; Glyco_hydro_28; 1. SMART; SM00710; PbH1; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; PbH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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VSGVQISDVTYEDIHGTSATEVAVKFDCSPKHPCREIKLEDVKLTYKN-QAAESSCSH
                             FSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKN
                                                                                                                                                                                                                                                                                                                                                                            FRIAGTLVAP---SDYRVIGNAANWIFFHHVNGVTI-SGGILDGQGTALW--ACKACHGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCR-SSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                             TVKTVTFSGTQNGLRIKSWGRPSTGFARNILFQHATMVNVENPIVIDQHYCPDNKGCPGQ
                                                                                                                   TVNEAKIIGAENGVRIKTW-QGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQ
                                                                                                                                                                                        VQMSSGVTILNSKIATGDDCVSIGPGTSNLWIEGVACGPGHGISIGSLGKEQEEAGVQNV
                                                                                                                                                                                                                                  VSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNV
                                                                                                                                                                                                                                                                                 SCPSGATTLGFSDSNNIVVSGLASLNSQMFHIVINDFQNVQMQGVRVSRSGNSPNTDGIH
                                                                                                                                                                                                                                                                                                                                PCRDAPTALTEWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVH
                                                                                                                                                                                                                                                                                                                                                                                                                        VKIFGSLEASSKISDYK---DRRIWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVASLGAKADGKTDSTKÄFLSAWAKACASMNPGVIYVPAG-TFFLRDVVFSGPCKNNAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 AA;
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYGALACTURONASE.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53DCC26944D22BF9
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pectate and other galacturonans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 4.1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 393;
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Matches
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CARBOHYD
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ACT SITE
CARBOHYD
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Q39786;
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15-JUL-1998
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U09717; AAA82167.1; PIR; S52006; S52006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA: tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosic
                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Coker 312; TISSUE=Poll
MEDLINE=95161720; PubMed=7858233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gossypium hirsutum (Upland cotton)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cotton (Gossypium hirsutum L.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               John M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro; IPR000743;
interPro; IPR006626;
                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           galactosiduronic linkages in pectate and other galacturo TISSUE SPECIFICITY: Pollen.

DEVELOPMENTAL STAGE: Appears 12 days before anthesis and levels are seen in pollen on the day of anthesis.

SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                during pollination.

CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nt Mol. Biol. 26:1989-1993(1994).
FUNCTION: May function in the depolymerizits walls during pollen tube elongation,
                                                        80
                                                                                                                                                                             140;
                                                                                                                                                67
                                                                                                                                                                                          Similarity
                                                                         SGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSC 186
                                                                                                                                                                                                                                                                                                                                                                                         PS00502;
CENREFRSK-LPVNIRFDFLTNALIQDITSKDSKLFHINVFACKNITLERLKIEAPDESP
                          KINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSP
                                                     EGPCKAPIEINVQGTIQAPADPSAFKDPN-WVRFYSVENFKMFGGGIFDGQGSIAYEKNT 138
                                                                                                                                              KVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITF
                                                                                                                   KVQSDAFDV--VAKFGAKADGKTDLSKPFLDAWKEACASVTPSTVVIPKG-TYLLSKVNL
                                                                                                                                                                                                                                                                                                                                                                        Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petersen M.W.;
                                                                                                                                                                                                                                         407
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3 (Rel. 36,
3 (Rel. 42,
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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y function in the depolymerization of the
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temporal specificity of its promoter in transgen
                                                                                                                                                                                                                                                                                                                                                                                         POLYGALACTURONASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor
                                                                                                                                                                                                                                       43921
                                                                                                                                                                          27.9%; Score 667; DF 38.4%; Pred. No. 1.26 tive 69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Glyco_hydro_28.
PbH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
cursor (EC 3.2.1.15) (PG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                           Cell
                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                  POLYGALACTURONASE.
BY SIMILARITY.
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                      wall; Signal; Glycoprotein
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                                                                                                                                                                                                                                         B81B2BC4C312D195
                                                                                                                                                                                        667; DB 1;
No. 1.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                        Length 407;
                                                                                                                                                                                                                                         CRC64;
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(POTENTIAL).
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                                                                                                                             RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottler P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Conrad A., Hornischer K., Kauer G., Loehnett T.-H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Rooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Mayer K.F. X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Mayer K.F. X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Mayer K.F. X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Pai G., Militscher J., Sellers P., Gill J.E., Feddblyum T.V.,

RA Pai G., Militscher J., Sellers P., Gill J.E., Feddblyum T.V.,

RA Pai G., Militscher J., Sellers P., Gill J.E., Feddblyum T.V.,

RA Rooney T., Kaneko T., Nakamura Y., Sator, Kato T., Asamizu E.,

RA Rooney T., Kaneko T., Nakamura Y., Sator, S., Kato T., Asamizu E.,

RA Rooney T., Kaneko T., Nakamura Y., Sator, S., Kato T., Asamizu E.,

RA Rooney T., Kaneko T., Nakamura Y., Sator, S., Kato T., Asamizu E.,

RA Kiyokawa C., Kohara M.
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01-FEB-1996 (Rel. 33, Created)
01-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Exopolygalacturonase clone GBGA483 precursor (EC 3 (Pectinase) (Galacturan 1,4-alpha-galacturonidase)
AT3G07850 OR F17A17.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARATH
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STRALN=CV. C24; TISSUE=Flower buds
MEDLINE=99413295; PubMed=10485285;
Torki M., Mandaron P., Thomas F.,
                                                                  Kiyokawa C., Kohara M., Matsumoto M., Matsuno
Nakayama S., Nakazaki N., Shinpo S., Takeuchi
Watanabe A., Yamada M., Yasuda M., Tabata S.,
"Sequence and analysis of chromosome 3 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Differential expression of a polygalacturonase Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosio
                                           "Sequence and thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
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A Southwick A.M., WH H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                     Query Match
Best Local :
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SEQUENCE FROM N.A.
STRAIN=cv. Columbia
STRAIN=72954850;
                                                                                                                                                                                                                                                                                                                                     ACT_SITE
CARBOHYD
CARBOHYD
CONFLICT
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Multigene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X72292; CAA51033.1; --
EMBL; AC013483; AAF21195.1; --
EMBL; AC056173; AAL07022.1; --
EMBL; AY091200; AAM14139.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 302:842-846(2003).
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                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00295; Glyco_hydro_28; SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
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                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \{(1,4)\text{-alpha-}D\text{-galacturonide}\}(N\text{-}1) + D\text{-galacturonate.} \\ \text{SUBCELLULAR LOCATION: Secreted.} \\ \text{SIMILARITY: Belongs to family 28 of glycosyl hydrolases.} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polygalacturonase.
CATALYTIC ACTIVITY: {(1,4)-alpha-D-galacturonide}(N)
('/ /)-alpha-D-galacturonide}(N-1) + D-galacturonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        development, germination,
168 VGGGGTI-NGNGQVWWPSS-CKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      Similarity
                                                  PVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLV
                                                                                                                                                                                                                      ILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNIDK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requires a license agreement
                                                                                                                   TAKNAATAVGGAAASVGAKVSGAKPGAAVDVKASGAKGDSKTDDSAAFAAAWKEACAAGS
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342
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Pred. No. 1.3e-39;
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; DF1D4C30FB1C3F11 CRC64;
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N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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and tube growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
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                                                                          ACT SITE CARBOHYD
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15-JUL-1998
15-JUL-1998
10-OCT-2003
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                                                                                                                                                                                                                                               Pfam; PF00295; Glyco_hydro_28; 1. SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                            EMBL; U09805; AAA58322.1; -
InterPro; IPR000743; Glyco_hydro
InterPro; IPR006626; PbH1.
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                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                         PROSITE; PS00502; POLYGALACTURONASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: May function in the depolymerization of the pectin in its walls during pollen tube elongation, or in that of the pistil during pollination.

CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               galactosiduronic linkages in TISSUE SPECIFICITY: Pollen (F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'ollen;
-95161720; PubMed=7858233;
3., Petersen M.W.;
(Gossypium hirsutum L.) pollen-specific polygalacturonase
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36, Last sequence update)
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J. Mol. Biol. 229:797-801(1993).
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01-JUN-1994 (Rel. 29, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation updat
Exopolygalacturonase precursor (EC 3.2.1.67
    modified
                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93164262; PubMed=8433375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4577;
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                                                                                                                                                                                      polygalacturonase.

CATALYTIC ACTIVITY: {(1,4)-alpha-D-galacturonide}(N) +

{(1,4)-alpha-D-galacturonide}(N-1) + D-galacturonate.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Pollen.
                 s SWISS-PROT entry is copyright. It is I seem the Swiss Institute of Bioinformat European Bioinformatics Institute. The European Bioinformatics as long
                                                                                                                                        DEVELOPMENTAL STAGE: Late stages SIMILARITY: Belongs to family 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missouri 17; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --VAKFGAKADGKTDLSKPFLDAWKEACASVTPSTVVIPKG-TYLLSKVNL
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Pred. No. 1.4e
69; Mismatches
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                                                                 ght. It is produced through a collaboration Bioinformatics and the EMBL outstation
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Best Local S
Matches 131
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01-MAR-1992
01-MAR-1992
10-OCT-2003
MEDLINE=93005658; PubMed=2152116;
Brown S.M., Crouch M.L.;
"Characterization of a gene family abundantly expressed organensis pollen that shows sequence similarity to polygalacturonase.";
                                                                                                                                                                                                                                                                                                                                                                                          OENOR
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ACT SITE
CARBOHYD
                                                                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Exopolygalacturonase (EC 3.2.1.67) (ExoPG) (Pectinase)
1,4-alpha-galacturonidase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires or send an email
                                                                                                                                                                              Oenothera organensis (Evening primrose).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid.

Myrtales; Onagraceae; Oenothera.
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SMART; SM00710; PbH1; 5.
PROSITE; PS00502; POLYGALACTURONASE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000743; Glyco
InterPro; IPR006626; PbH1.
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Pred. No. 1.7e-38;
5; Mismatches 143
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N-LINKED (GLCNAC. ..) (PO
N-LINKED (GLCNAC. ..) (PO
SBD1310F588AE7CA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  щ
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                                                                                                                                                                                                                                                                                                                                                                         A
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(POTENTIAL)
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Query Match
Best Local S
Matches 129
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Hydrolase; Glycosic
NON TER 1
ACT SITE 202
CARBOHYD 140
CARBOHYD 192
CARBOHYD 192
CARBOHYD 192
CARBOHYD 225
SEQUENCE 362 AA;
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-!- FU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polygalacturonase. -i- CATALYTIC ACTIVITY: \{(1,4)-alpha-D-galacturonide\}(N) + H(2)0 -i- CATALYTIC ACTIVITY: \{(1,4)-alpha-D-galacturonide\}(N-1) + D-galacturonate (1,4)-alpha-D-galacturonide \{(1,4)-alpha-D-galacturonide \}(N-1) + D-galacturonate discount of the style of the specific of the style of the specific of the style of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the specific of the s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               during germination and tube growth.
-!- SIMILARITY: Belongs to family 28 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pollination.
-i- DEVELOPMENTAL STAGE: Accumulates late
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rt Cell 2:263-274(1990). FUNCTION: May function in
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302
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                                                                                                                                                                        332
                                                      392
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KEAVKLVCSKSFPCNGVELADIDLTYSGKGGPATSVCENI
                                                         KVAIKFDCSTNFPCEGIIMENINLV-GESGKPSEATCKNV
                                                                                                               KSEPGEASEMHFQDITMNSVGTPILIDQGYCPYNQCTAEVPSSVKLSKISFKNIKGTSTT
                                                                                                                                                                  QGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSAT
                                                                                                                                                                                                                              ISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTW-
                                                                                                                                                                                                                                                                                                                                                DVTTLDSKNFHVNVIGCKNLTFERFKISAAETSINTDGIHIGRSDGVNIINTEIKTGDDC
                                                                                                                                                                                                                                                                                                                                                                                                      NLKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKD
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IPR006626; PbH1.
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192
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225
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N-LINKED (GLCNAC...

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PRESULT 13
PGLR MAIZE
ID PGLR M
AC P26216
DT 01-MAY
DT 10-OCT
DE EXOPO1
DE EXOPO1
DE GALAC
GN PG1 AM
OS Zea ma
OC EMKARY
OC SPETRA
OC SPETRA
OC SPETRA
RN (1)
RN (1)
RP SEQUEN
RC STRAIN
                                                                                                                 P26216;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Exopolygalacturonase precursor (EC 3.2.1.67)
(Galacturan 1,4-alpha-galacturonidase).
PG1 AND PG2 AND PG3 AND PG6 AND PG14.
                                      Spermatophyta; Magnoliophyta;
PACCAD clade; Panicoideae; And
NCBI TaxID=4577;
 SEQUENCE FROM N.A., STRAIN=cv. Missouri
                                                                                     Eukaryota;
                                                                                                                                                                                                                          PGLR MAIZE
                                                                                                   Zea mays (Maize)
                                                                                        Viridiplantae;
                                                                                                                                                                                                                          STANDARD;
AND
17;
 SEQUENCE OF 23 TISSUE=Pollen;
                                                                        Streptophyta; En
<sub>Y</sub>ta; Liliopsida;
                                                         Andropogoneae;
                                                                                                                                                                                                                          PRT;
               23-37
                                                                                                                                                                                                                          410
                                                                                      Embryophyta;
                                                                                                                                                                                                                          A
                                                            Zea
                                                                          Poales;
                                                                                                                                                 (ExoPG)
                                                                           Poaceae;
                                                                                      Tracheophyta;
                                                                                                                                                   (Pectinase)
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EMBL; X57627; CAA40850.1; -...

EMBL; X57628; CAA40851.1; ALT_

EMBL; X57743; CAA40803.1; -...

EMBL; X57575; CAA40803.1; -...

EMBL; X65844; CAA46679.1; -...

EMBL; X65845; CAA46680.1; -...

EMBL; X62384; CAA4248.1; -...

EMBL; X62385; CAA4249.1; -...

EMBL; X62385; CAA42234.1; -...
                                                                                                                                                                                     PIR; S18570; S18570.
PIR; S25824; S25824.
PIR; S30064; S30064.
MaizeDB; 25864; -.
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Plant M
                            ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allen R.L., Lonsdale P...., "Sequence analysis of three members of the maize pgene family expressed during pollen development."; plant Mol. Biol. 20:343-345(1992).
                                            CHAIN
ACT_S
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-306 FROM N.A.

MEDLINE-94035141; PubMed-8106080;

Allen R.L., Lonsdale D.M.;

"Molecular characterization of one of the maize gene family members which are expressed during l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Missouri 17, TISSUE=Leaf;
MEDLINE=93164262; PubMed=8433375;
Barakate A., Martin W., Quigley F., Mache R.;
"Characterization of a multigene family encoding exopolygalacturonase in maize.";
  CARBOHYD
                                                                          SIGNAL
                                                                                                     Hydrolase;
                                                                                                                  PROSITE; PS00502;
                                                                                                                              Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
                                                                                                                                                          InterPro; IPR000743; Glyco_hydro_
InterPro; IPR006626; PbH1.
                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development.
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MEDLINE=93004490; PubMed=139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of pollen polygalacturonase clones in maize.";
Plant Mol. Biol. 17:1155-1164(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Niogret M.F., Dubald M., Mandaron "Charactoria"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polygalacturonase.

CATALYTIC ACTIVITY: {(1,4)-alpha-D-galacturonide}(N)

((1,4)-alpha-D-galacturonide}(N-1) + D-galacturonate.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Pollen.

DEVELOPMENTAL STAGE: Late stages of pollen developmen

SIMILARITY: Belongs to family 28 of glycosyl hydrolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: May function in depolymerizing pectin development, germination, and tube growth. Acts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3:261-271 (1993)
                                                                                      family.
                                                                                                   Glycosidase;
  1
23
256
89
246
349
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Lonsdale D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229:797-801(1993).
                                                                                   MI; s.
POLYGALACTURONASE; 1.
POLYGALOUTH wall; Signal; Glycoprotein;
 210
256
256
246
349
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                                                                                                                                                                                                                                                                                                                                          ALT_INIT.
EXOPOLYGALACTURONASE.
PROBABLE.
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of pollen development. of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the maize polygalacturonase
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late pollen
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MEDLINE=93164262; PubMed=8433375;
Barakate A., Martin W., Quigley F., Mache R.;
"Characterization of a multigene family encoding exopolygalacturonase in maize.";
J. Mol. Biol. 229:797-801(1993).
-i- FUNCTION: May function in depolymerizing pect
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01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Exopolygalacturonase precursor (EC 3.2.1.67)
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                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Q40312;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG
Medicago sativa (Alfalfa)
                                                                                                                                                                                               MEDSA
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SMART; SM00710; PbH1; 5.
PROSITE; PS00502; POLYGALACTURONASE;
Hydrolase; Glycosidase; Cell wall; Si
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                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago
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Multigene
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InterPro; IPR006626; PbH1.
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 SEQUENCE FROM N.A. STRAIN=CV. C2-4; T
                                        NCBI_TaxID=3879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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Pred. No. 8.9e-37;
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1995) to the depolymerization of the FUNCTION: May function in the depolymerization of the its walls during pollen tube elongation, or in that o during pollination (By similarity).
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galact-!- TISSUE SPECIFICITY: Pollen specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U20431; AAA62286.1; -.
PIR; T09398; T09398.
InterPro; IPR000743; Glyco_hydro_InterPro; IPR006626; PbH1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00295; Glyco hydro 28; 1.
SMART; SM00710; PbH1; 4.
PROSITE; PS00502; POLYGALACTURONASE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases
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LNNVDL-KFNGAPTTAKCTNV
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                                                                                                                                                                FTITAPGDSPNTDGIHMGKSTDVKILNTNIGTGDDCVSIGDGSKQITVQGVNCGPGHGLS
                                                                                                                                                                                        LMINASAKSENTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGEGHGIS
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

45	44	43	42	41	40	39	38	37	96	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
715	715.5	718	718	718.5	719.5	726	727	728	728	730	734	736	741.5	749.5	764	787.5		788	788.5	æ	25.		98.	$\vdash$	N	œ	1014	N
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392	397	435	351	395	398	392	392	443	405	392	503	423	491	1161	507	514	434	457	514	514	435	468	459	444	452	444	429	422
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
080559	Q9ZT65	Q9LYJ5	Q84N55	022610	Q8GTP7	Q96487	Q40135	Q9SWS3	022818	022311	Q94IZ1	081245	Q9FWX5	Q9LQD1	<b>61736</b> 0	886H8Ö	Q9FXC1	Q9ZUE7	Q8H989	Q8H987	Q9SLP3	Q9CAL5	Q9SSC2	Q94AJ5	Q9M7D3	Q84M40	Q84ZN9	Q84ZP5
080559 arabidopsis	Q9zt65 lycopersico	Q9lyj5 arabidopsis	Q84n55 prunus pers	O22610 lycopersico	Q8gtp7 pyrus commu	Q96487 lycopersico	Q40135 lycopersico	Q9sws3 glycine max	O22818 arabidopsis	lycop	oryza	cucum:	arabidopsi	arabidopsi	Q9fy19 juniperus a	Q8h988 cryptomeria	Н	arabidopsi		Q8h987 cryptomeria	Q9slp3 cucumis sat	Q9cal5 arabidopsis	Q9ssc2 arabidopsis		lycopersi	oryza sat	9 oryza	Q84zp5 oryza sativ

## ALIGNMENTS

DR DR DR DR SQ	DR DR	R R R R	388	333	RRX	RC RP	<b>2</b> 2 2 2	888	G G		D I	Q9M6S2 ID Q	RESULT
InterPro, IPR000408; Reg_chx condens.  Pfam; PR00295; Glyvo_hydro_28; 1.  SMART; SM00710; PbHI; 4.  SMART; SM00710; PbHI; 4.  SMOOS1TE; PS00502; POLYGALACTURONASE; 1.  PROSITE; PS00626; RCC1_2; 1.  Cell wall; Glycosidase; Hydrolase.  SEQUENCE 463 AA; 50352 MW; 7EED7EEFE54988FA CRC64;	GO:0005975; erPro; IPR000 erPro; IPR006	EMBL; AFI-12758; AAF71160.1; GO; GO:0005618; C:cell wall; IEA. GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA. GO; GO:0016798; F:polygalacturonase activity; IEA.	Plant Mol. Biol. 42:317-328(2000)!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES	"Polygalacturonase gene expression in kiwifruit: relationship to fruit softening and ethylene production.";	MEDLINE=20252524; PubMed=10794531; Wang Z.Y., MacRae E.A., Wright M.A., Bolitho K.M., Ross G.S.,		Ericales; Actinidiaceae; Actinidia. NCBI TaxID=3625; Ini —	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	PGA.  Actinidia chinensis (Kiwi) (Vangtao)	Last	01-OCT-2000 (TramBirel. 15, Created) 01-OCT-2000 (TramBirel. 15, Last sequence update)	9M6S2; PRELIMINARY;	LT 1

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RESULT

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Best Local Similarity
Matches 256; Conserv
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Q1-DEC-2001 (TYEMBLYel. 1
Q1-DEC-2001 (TYEMBLYel. 1
Q1-JUN-2003 (TYEMBLYel. 2
Polygalacturonase PG1.
Vitis vinifera (Gyape)
                                                                        EMBL; AY043233; AAK81876.1; -.
G0; G0:0005618; C:cell wall; IEA.
G0; G0:0016798; F:hydrolase activity, acting on glycosyl
G0; G0:0014650; F:polygalacturonase activity; IEA.
G0; G0:0005975; P:carbohydrate metabolism; IEA.
Interpro; IPR000743; Glyco_hydro_28.
Interpro; IPR000743; Glyco_hydro_28.
Interpro; IPR0006626; PbH1.
Interpro; IPR0006626; PbH1.
Interpro; IPR0006626; DH1.
SMART; SM00710; DbH1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Shiraz;
Nunan K.J., Davies C., Robinson S.P., Fincher G.B.;
"Characterization of cell wall modifying enzyme active
corresponding cDNAs during grape berry development.";
                                                                                                                                                                                                                                                                                                                                       Planta 0:0-0(2001).
-i- SIMILARITY: BELONGS TO FAMILY 28
(POLYGALACTURONASES).
                             PROSITE; PS00502; POLYGALACTURONASE; PROSITE; PS00626; RCC1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                             Planta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Vitaceae; Vitis.
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        Glycosidase; Hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                     GLYCOSYL HYDROLASES
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PRESULT 3

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Query Match
Best Local Similarity
                                                                           EMBL; AF434714; AAL30418.1; -.
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; E:hydrolase activity, acting on gl:
GO; GO:0016798; E:hydrolase activity, IEA.
GO; GO:0004650; F:polygalacturonase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; bbH1.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; bbH1; 6.
PROSITE; PS00502; POLYGALACTURONASE; 1.
Cell wall; Glycosidase; Hydrolase.
SEQUENCE 428 AA; 45830 MM; F553DBA6C297626D CR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                   Christiansen L.C., Dal Degan F., Ulvskov P., Borkhardt E "Examination of the dehiscence zone in soybean pods and dehiscence-related endopolygalacturonase gene."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases-i- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLZ (POLYGALACTURONASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q944B5;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation updat
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49.6%;
51.5%;
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Score 1185.5; DB 10;
Pred. No. 1.3e-69;
                                                                                    F553DBA6C297626D CRC64;
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GO; GO:0005518; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, acting on
GO; GO:0004550; F:polygalacturonase activity; IE
GO; GO:0004550; F:carbohydrate metabolism; IEA.
Interpro; IPR000743; Glyco_hydro_28.
Interpro; IPR000408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.

SMART; SM00710; PBH1; 4.
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Q9SFB7;
01-MAY-2000
                                                                                                                                                                                                                                                                          Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC F17A17 genomic seq Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                   PROSITE; PS00502; POLYGALACTURONASE; PROSITE; PS00626; RCC1_2; 1. Cell wall; Glycosidase; Hydrolase.
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EMBL; AY078936; AAL84942 1; -.
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, actir
GO; GO:0014650; F:polygalacturonase activit
GO; GO:0005975; P:carbohydrate metabolism;
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR0006656; PbHL.
InterPro; IPR000408; Reg_chr_condens.
                                                                                                                                                                                      "Arabidopsis cDNA clones.";
Submitted (FEB-2002) to the
-!- SIMILARITY: BELONGS TO I
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Query Match
Best Local Sin
Matches 226;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Endopolygalacturonase.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Str
Spermatophyta; Magnoliophyta;
eurosids II; Brassicales; Bra
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PROSITE; PS00626; RCCL 2; 1.
Cell wall; Glycosidase; Hydrolase.
Cell wall; Glycosidase; Hydrolase.
SEQUENCE 433 AA; 46492 MW; 08E1EE62AA05A26B CRC64;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica napus (Rape).
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; SM00710; PbH1; 5.
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                                                                                                                                                                                                                                                                                                                                                                                   Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots; rosid Brassicaceae; Brassica.
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Pred. No. 3.2e-67
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"Polygalacturonase gene expression in ripe melon frustr for polygalacturonase in ripening-associated pectin L plant Physiol. 116:0-0(1998).

C --- SHIMLARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYD.
C (POLYGALACTURONASES).

R EMBL, AF062467; AAC26512.1; --
R PIR; T08215; T08215.

GO; GO:0005618; C:cell wall; IEA.

GO; GO:0016798; F:hvdrrl---
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Best Local (
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01-NOV-1998
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR000628; PbH1.
InterPro; IPR0006028; PbH2.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
PROSITE; PS00502; POLYGALACTURONASE; 1.
PROSITE; PS00626; RCC1_2; 1.
Cell wall; Glycosidase; Hydrolase.
SEQUENCE 434 AA; 46603 MW; E9249ACLBEC0C219
                                                                                                                                                                                       Cucumis melo (Muskmelon).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                  081246
                                                                                                                                                                                                                                                  MPG3
                                                                                                                                                                                                                                                            Polygalacturonase
                                                                                                                                                                                                                                                                                                                     081246;
                                                                                                                                                                           NCBI_TaxID=3656;
                                                                                                                                                                                                                                                                                                                                                                                                                                  421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RINGPCKSYLTVQILGTISASQQRSDYEDLSKWITFDGVNSLTVDGGATGTVNGNGAET 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GTINGNG-QV 180
                                                                                                                                                                                                                                                                                                                                                                                                      --GKASCSNANVMDKDGVLPQCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                  KPSEATCKNVHFNNAEHVTPHCTS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APADSPNTDGIHITNTQNIQVSNSIIGTGDDCISIESGSQNVQINDLTCGPGHGISIGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             YCDK-SKCTEQKSAVQIKNVVYRNISGTSASDIAITFNCSKNYPCQGIVLDKVNIKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDDNSKAFVSGVTVDGAKLSGTDNGVRIKTNQGGSGTASNIIFQNIQMENVENPIIIDQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVDKNGIKV----INVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQ 123
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                                                                                                                                                                                                                                                                        (TrEMBLrel. 08, 1 (TrEMBLrel. 24, 1
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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49.88;
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Last annotation updat
                                                                                                                                                                                                                                                                                                      Created)
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Pred. No. 5.6e-66;
78; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                  PRT;
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    glycosyl bonds;
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                                                                                                    disassembly.";
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Best Local S
Matches 224
                Submitted [2]
                                                                                   SEQUENCE FR
STRAIN=cv.
                                                                                                                                                                                                                                                                                                                           023147;
                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Endo-polygalacturonase (At3g57510).
PGA1 OR ADPG1 OR T8H10.110 OR AT3G57510/T8H10_110.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core
eurosids II, Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004650; F:polygalacturonase activity; I GO; GO:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR000743; Glyco hydro_28. InterPro; IPR006626; PbH1. InterPro; IPR000408; Reg chr condens. Pfam; PF00295; Glyco hydro_28; 1.
SMART; SM00710; PbH1; 4.
                                                    Sander L.,
Borkhardt
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PROSITE; PS00626; RCC1 2; 1.
Cell wall; Glycosidase; Hydrolase; Sign Cell wall; Glycosidase; Hydrolase; Sign SIGNAL 1 34
SEQUENCE FROM N
                                                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
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                                                                   E FROM N.A.
cv. COLOMBIA;
c., Child R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFLFVVVVNFDTFSTCFGSYPDVDNPLPSISSGDKEDYGQHYYEHSSSEFSSMLRT--RL
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                                   (OCT-1997)
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50697 MW;
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50.2%;
                                   to
                                                                     Ulvskov P.,
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                                   EMBL/GenBank/DDBJ databases
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Pred. No. 8
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edons; core e
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                                                                     Joergensen
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                                                                                                                                                                                                Tracheophyta;
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Mayer K.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Chan M.M., Chang C.H., Kamiya A., Karlin-Neumann G., Kawai J., Lam Lishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005618; C:cell wall; IEA.
GO; GO:0005618; F:bydrolase activity, acting on glycosyl bonds;
GO; GO:0004650; F:polygalacturonase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR000626; PbH1.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
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Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
Seki M., Iida K., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jenkins E.S., Roberts J.A.;
"Dehiscence-related expression of an Arabidopsis thaliana gene
"Dehiscence-related expression of an Arabidopsis thaliana gene
encoding a polygalacturonase in transgenic plants of Brassica napus.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00502; POLYGALACTURONASE; 1.
PROSITE; PS00626; RCC1_2; 1.
Cell wall; Glycosidase; Hydrolase; Sign
CEQUENCE 431 AA; 46572 MW; 0F0F30DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palm C.J., Quach H.L., Sak
Tang C.C., Toriumi M., Won
Shinozaki K., Davis R.W.,
"Arabidopsis ORF clones."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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INGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
                                                            GKTYLLKSTRFRGPCKSLRNFQILGTLSASTKRSDYKDKNHWLILEDVNNLSIDGGSTGI
                                                                                           NKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GT
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.X., Queti
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                                                                                                                                                                                                                                                                                                  71;
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                                                                                                                                          -TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLVPK
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ka M., Carninci
                                                                                                                                                                                                                                                           -DNLFKQVYDNILEQEFAHDFQAYLSYL
                                                                                                                                                                                                                                                                                                                                        DB 10;
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nci P.,
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Kawai
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MEDLINE=20083487; Pubmed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
                                                                                                                                                                                                                                                                                 GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:bydrolase activity, acting on glycosyl
GO; GO:001650; F:polygalacturonase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; pbH1.
InterPro; IPR006826; pbH1.
InterPro; IPR006826; pbH1.
SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES (POLYGALACTURONASES).
EMBL; AC002339; AAC02763.1; -.
EMBL; H84846; H84846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                             PROSITE; PS00502; POLYGALACTURONASE; PROSITE; PS00626; RCC1_2; 1.
Cell wall; Glycosidase; Hydrolase.
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Submitted (MAR-1996) to the EMBL/GenBank/DBJ databas -: SIMMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDE (POLYGALACTURONASES).

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  SEQUENCE FROM N.A. STRAIN=cv. Maravil Speirs J.;
                                                                                    Lester D.R., Speiers J., Orr G., Brady C.J., "Peach (Prunus persica) endopolygalacturonase - analysis in melting and nonmelting peach cultiva plant Physiol. 105:225-231(1994).
                                                                                                                                                                               MEDLINE=94302167; PubMed=8029352;
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STRAIN=cv. Maravilla;
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433 AA; 46595 MW; 1EDB29AC3B958260 CRC64;
                            Maravilla;
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Best Local
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Q8VXT3;
01-MAR-2002
01-OCT-2002
01-JUN-2003
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SMART; SM00710; PBH1; 6.
PROSITE: become
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PROSITE; PS00626; RCCL_2; 1.
Cell wall; Glycosidase; Hydrolase.
SEQUENCE 458 AA; 49716 MW; E7BAB!
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SEQUENCE FROM N
Rodriguez-Gacio
                                                                                         Brassica rapa (Turnip).

Bukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Brass:
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InterPro; IPR006626; PbH1.
InterPro; IPR000408; Reg_chr_condens
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                                                                   NCBI_TaxID=51350;
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GO:0016798; F:hydrolase activity, activit
GO:0004650; F:polygalacturonase activit
GO:0005975; P:carbohydrate metabolism;
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SIMILARITY: BELONGS
(POLYGALACTURONASES)
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                                                                                                                                                                                                          polygalacturonase
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3 (TrEMBLrel.
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Last annotation updat
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Pred. No. 1
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                                                                                                Brassica
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eudicots;

Tracheophyta;

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Length Indels

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Best Local S
Matches 222
                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid. eurosids II; Brassicales; Brassicaceae; Brassica. NCBI—TaxID=3708;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES (COLYGALACTURONASES).
EMBL; AJ428543; CAD21651.2; -...
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; GO; GO:0004650; F:polygalacturonase activity; IEA.
GO; GO:0004575; P:carbohydrate metabolism; IEA.
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InterPro; IPR000408; Reg chr condens.
Pfam; PF00295; Glyco hydro 28; 1.
PROSITE; PS00502; POLYGALACTURONASE; 1.
PROSITE; PS00626; RCC1 2; 1.
Cell wall; Glycosidase; Hydrolase.
                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         Polygalacturonase
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       Characterization and
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Last sequence update)
Last annotation update)
(EC 3.2.1.15).
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    polygalacturonase
                        Roberts J.
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QRGTPB ID QRGTP AC QRGTP AC QRGTP O1-MA DT 01-MA DT 01-OC GEVEUS OC ENKAZ OC SPEUS OC SPEUS OC SUCH CON NCBI RN [1]
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R GO; GO:0005618; C:cell wall; IEA.

R GO; GO:0016798; F:hydrolase activity, acting on glycc
R GO; GO:001650; F:pollygalacturonase activity; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

JR InterPro; IPR000743; Glyco_hydro_28.

JR InterPro; IPR006626; PbH1.

DR InterPro; IPR006626; Reg_thr_condens.

DR Pfam; PF00295; Glyco_hydro_28; 1.

SMART; SM00710; PbH1; 6.

DR SMART; SM00710; PbH1; 6.
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Best Local
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Q8GTP8;
01-MAR-2003 (TrEMBI
01-MAR-2003 (TrEMBI
01-OCT-2003 (TrEMBI
Polygalacturonase p
PC-FG1.
Pyrus communis (Pear).
Pyrus communis (Pear).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids 1; Rosales; Rosaceae; Maloideae; Pyrus.
NCBI TaxID=23211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                during pod development in oilseed rape (Brassica napus L.).";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00502; POLYGALACTURONASE; 1.
PROSITE; PS00626; RCCl 2; 1.
Cell wall; Glycosidase; Hydrolase; Signal.
SIGNAL 1 25 POTENTIAL.
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                                                                                                                                                                                                                                                                                  QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE
|||||::|:||:||:||:||
QNYCDK-DKCEQQESAVQVNNVVYRNIQGTSATDVAIMENCSVKYPCQGIVLENVNIKG-
                                                                                                                                                                                                                                                                                                                                                       SLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIID
                                                                                                                                                                                                                                                                                                                                                                                          QVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GKASCKNVNVKDKGTVSPKC
                                                                                                                                                                                                                                                        SGKPSEATCKNVHFNNAEHVTPHC 442
                                                                                                                                                                                                                                                                                                                                      SLGDDNSKAYVSGINVDGATLSETDNGVRIKTYQGGSGTAKNIKFQNIRMDNVKNPIIID
                                                                                                                                                                                                                                                                                                                                                                                                        INASAKSPNIDGVHVSNIQYIQISDTIIGTGDDCISIVSGSQNVQATNIICGFGHGISIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIWWQNSCKIDKSKPCTKAPTALTLYNLNNLNVKNLRVRNAQQIQISIEKCNSVDVKNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIFLCVLLMLACCQALSSNVDDGYGHEDGSFET--DSLIKLNNDDDVLTLKSSDRPTTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILLLIIIFASSISTCRSNVID-----DNLFKQVYDNILEQEFAHDFQAYLSYLSKNIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
433 AA;
                                                                                                      (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 25,
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLIPKGKTYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46670 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1103; DI
Pred. No. 3.2e
70; Mismatches
                                                                                           Last sequence up Last annotation (EC 3.2.1.15).
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POLYGALACTURONASE.
                                                                                                                                                              PRT;
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                                                                                                                       update)
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Best Local S
Matches 224
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Hiwasa K., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
GO; GO
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Submitted
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SIGNAL 1 24 PO
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InterPro; IPR006626; PbH1.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid eurosids I; Rosales; Rosaceae; Rosoideae; Rubus.
                                                                                                                    O65886;
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00502; PCLYGALACTURONASE; PROSITE; PS00626; RCC1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                         Rubus idaeus (Raspberry).
Eukaryota; Viridiplantae;
                                                                                          01-AUG-1998
01-JUN-2003
                                                                               Polygalacturonase
                                                                                                                                              065886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; AB084461; BAC22688.1; -G0:0016798; F:hydrolase activity, acting on glycosyl G0:0004650; F:pdygalacturonase activity; IEA.G0:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                               276
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24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            WIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLFC-RDAFTALTFWNCKNLKVNNLK
                                                                                                                                                                                                                                     IKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHC
                                                                                                                                                                                                                                                                              GQASNIKFLNVEMQDVKYPIIIDQNYCD-RVEPCIQQFSAVQVKNVVYENIKGTSATKVA
                                                                                                                                                                                                                                                                                                                                     V$G$QNVQATNITCGPGHGISIG$LG$GN$EAYV$NVTVNEAKIIGAENGVRIKTWQGG$
                                                                                                                                                                                                                                                                                                                                                                                                                             WILLEDNVONLLVVGPGTINGSGNIWWKNSCKRKPQPPCGTHAPTAVTFNRCNNLVVKNIK
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KAWKAACSSSGAIVLVVPQ-KKYLVRPIDFSGPCKSQLTVQIYGTIEASEDRSIYKDIDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEGLKFMELIRPRTQLSSSRKLNTI-TGGIATSSAPAKTISVDDFGAKGNGAD-DTQAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALKTQLLWSFVVVFVVSFSTTSCSGSSFQEVNALHSYVDHVDDRVSGYNSRAYPSYMDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVIQRNSILLLIIIFASSIST--CRSNVIDD-NLFKQVYDNILEQEFAHDFQAYLSYLS-
                                                                                                                                                                                                              ITLNCSQSVPCRGIALQSVRL--QNGR---AECNNVQPAYKGVASPRC
                                                                                                                                                                                                                                                                 GSATNI VFONVOMNNVTNPII I DONYCDHKTKDCKOOKSAVOVKNVLYONI RGTSASGDA
                                                                                                                                                                                                                                                                                                                                                                         IQDAQQMHVRFQNCINVQASRLTVTAPEDSPNTDGIHVTNTQNITISSSVIGTGDDCISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRL
                                                                                                                                                                                                                                                                                                                      {\tt VSGSQRVQATDITCGPGHGISIGSLGEDGSKDHVSGVCVNGAKLSGTSNGLRIKTWQGGS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is required for both the initiation and progre
in pear (Pyrus communis L.) fruit.";
(MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROM N.A.
. La France;
. Kinugasa Y.
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                                                                                          (TrEMBLrel.
                                                                                                                    (TrEMBLrel.
                                                                                                                                              PRELIMINARY;
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., Amano S., Hashimoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNIESNNNIDKVDKNGI----
                                                                                          07, Created)
07, Last sequence up
24, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1073; DB 10;
Pred. No. 3.2e-62;
B; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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Best Local Similarity
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00502; POLYGALACTURONASE; PROSITE; PS00626; RCC1_2; 1. Cell wall; Glycosidase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; PbH1.
InterPro; IPR000408; Reg_chr_condens.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ224147; CAA11846.1; --
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl
GO; GO:0004650; F:polygalacturonase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1998) to the EMBL/GenBank/DDBJ-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
[1]
STRAIN=cv. Glen Clova; TISSUE=Fruit;
STRAIN=cv. Davies H.V., McNicol R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression of three genes up-regulated (Rubus idaeus cv. Glen Clova).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POLYGALACTURONASES
                                                                                                                                                                                                                                                                                              112 VVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGG
306
                                                     246
                                                                                 350
                                                                                                            186
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                                                                                                                                                                                                                         66
                                                                                                                                                                                                                                                                              7 LVPK-KNYLVKPITFSGPCKSKLTMQIYGSIEASDDRSVYSKDLYHWIIFDNVRNLLVQG
                                                                                                                                                                                                                                          GGTINGNGQVWWPSSCKINKSLPCRD-APTALTFWNCKNLKVNNLKSKNAQQIHIKFESC
                          IIMENINLYGESGKPSEATCKNVHFNNAEHVTPHC
                                                                        DVKYPIIIDQNYCDRVE--PCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEG
                                                                                                            GPGHGISIGSLGEGGSEDRVSKVTVNGAKISGTMNGVRIKTWQGGSGMASNIVFQNIEMN
                                                                                                                            GPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSSQASNIKFLNVEMQ
                                                                                                                                                         TNVQASYLTVTAPETSENTDGIHVANTQNITISNSIIGIGDDCISIVSGSQNVQASSITC
                                                                                                                                                                                   TNVVASNIMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITC
                                                                                                                                                                                                                         PGTINGNGQIWWQNSCKNKHTKPCGTLAPTAVTFYQCNNLVVKNLKFKDSQQMHVSFEDC
                                                     DVTNPIIIDQNYCDTSDKRKCKQQSKAVKVQNVLYKNIRGTSASKYAIAFDCSKSIPCQG
              ::
                                                                                                                                                                                                                                                                                                                                                                                           335
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                           AA; 36432 MW;
                                                                                                                                                                                                                                                                                                                                                  44.4%; 62.1%;
 HKRAKCSNVNLAYKENVSPRC
                                                                                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                    Score 1061.5; DB 10
Pred. No. 1.2e-61;
Pred. No. 1.7e-61;
                                                                                                                                                                                                                                                                                                                                                                                           B8BDFC7A85B6CDBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taylor M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in ripening
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                            442
 334
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Search completed: July Job time: 77.4797 secs 21, 2004, 17:08:12

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Minimum Maximum
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Perfect score:
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seq length: 2000000000
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1:    geneseqp1980s:*
2:    geneseqp1990s:*
3:    geneseqp2000s:*
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50
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1360.306 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	0	ر ت	4	w	2	٢	Result No.
		36						36		36			37	37	37			39	39	40		48	48	48	Score
70.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	74.0	•		74.0		76.0	78.0	78.0	0	٠	96.0	96.0	96.0	Query Match
10	2248	1284	1018	1018	1018	887	420	296	220	175	141	1038	582	568	443	149	427	449	321	979	10	10	10	10	Length
IJ	4	ப	δ	4	4	თ	υ	4,	4	σ	ហ	თ	4	σ	4	w	4	N	4	Ç	4.	ω	N	Ν	DB
ABB76722	ABB64494	AAP81187	ABJ18922	AAU34301	AAU37245	ABU21462	ABP73816	ABB65333	ABB71175	ABR52643	ABB83327	ABU15903	ABB59482	ADA07853	ABB61160	AAY44604	ABB61028	AAW18210	AAB70839	ABP35664	AAB48353	AAB19329	AAW10696	AAR45389	ID
Abb76722 Peptide l	4,	7	Abj18922 Pathogen	Aau34301 Staphyloc	ū	21462	Abp73816 Candida a	Abb65333 Drosophil	Abb71175 Drosophil	Abr52643 Protein s			Abb59482 Drosophil		Abb61160 Drosophil	Aay44604 Maize MLO	Abb61028 Drosophil	Aaw18210 Cellulomo	39	Abp35664 Fungal ZB	53	Aab19329 Polygalac	Aaw10696 Tomato po	45389 PG be	Description

45	44	43	42	41	40	39	38	37	36	35	34	ယ္	32	31	30	29	28	27	26
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525	495	463	455	424	411	328	246	232	219	219	219	218	208	206	202	125	121	86	19
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ABU36839	ABG93381	ABB71163	AAB81952	ADB07282	ADB07280	ABP73597	ABB64176	AAW63114	ABP65128	ABB83328	AAW93864	AAY17483	ABU70397	ABB83329	ABB61097	ABJ25282	AAY17484	ABP34678	AAW80371
	Abg93381 C. a	Abb71163 Dros	Aab81952 Pea	Adb07282 Allo	Adb07280 Allo	Abp73597 Cand	Abb64176 Dros	Aaw63114 A hu	Abp65128 Hypo	Abb83328 Human	Aaw93864 Human	Aay17483 Mur:	Abu70397 Human	Abb83329 Muri	Abb61097 Dros	Abj25282 Mouse	Aay17484 Human	Abp34678 Human	Aaw80371 Vasc
Protein e	albica	sophil	Pea bligh	Alloiococ	Alloíococ	Candida a	Drosophil	A human a	Hypoxia-r	an TSA	an BNI	Murine Ni	an adi	Murine TS	Drosophil	se BAC	an Nix		Vasopress

## RESULT 1 AAR45389 AAR45389 standard; protein; 10 ĄΑ

ALIGNMENTS

25-MAR-2003 06-JUL-1994 AAR45389; PG beta subunit internal fragment. (revised)
(first entry)

Beta subunit; PG; polygalacturonase; tomato; pathogen.

Lycopersicon esculentum

08-MAY-1992; 07-MAY-1993; 05~JAN-1994. EP577252-A1. Misc-difference 92US-00880915. 93EP-00303533 Location/Qualifiers /note= "unknown"

(UYAR-) UNIV ARIZONA STATE.

WPI; 1994-009528/02. Dellapenna D;

Transgenic tomato plants contg. lowered levels of polygalacturonase isoform 1 - for prodn. of tomatoes less susceptible to pathogens and requiring less energy to inactivate poly-galacturonase activity.

Example; Page 6; 15pp; English.

\$\times \times \ N-terminal sequence analysis of purified PG beta-subunit was performed. Two internal fragments (AAR45389-90) were used for the construction of primers (AAQ54493-95). Two beta-subunit cDNA clones and fragments of 11 others were sequenced. The consensus DNA sequence obtained is given in AAQ54492. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 10 AA;

96.0%; Score 48; DΒ 2 Length 10;

Query Match

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                                                                                                                                                                                                                                                                                                                                             AAW10696 and AAW10697 are internal peptides of the beta subunit of tomato polygalacturonase isoform 1 (PG1). The two peptides were generated by digestion with Lys-C and Gly-C endoproteases respectively. The peptides were used for the design of degenerate PCR primers used for cDNA library screening. A cDNA molecule encoding PG1 was identified, this sequence was used to produce constructs, antisense to the PG1 coding sequence, which are used to transform a tomato plant cell so as to reduce or eliminate PG1 activity. There are two isoforms of tomato polygalacturonase (PG), PG1 and PG2. PG1 has a much higher heat stability level (usually at least by 20 deg. C.) than PG2. By reducing or eliminating PG1 expression, leaving the less heat-tolerant isoform PG2. The process for production of tomato pastes, sauces etc. becomes less costly due to a lower temperature being needed for PG breakdown. A higher viscosity is also produced due to increased soluble pectin content. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic tomato plants with low level of polygalacturonase isoform 1 - have higher content of soluble pectin(s) and require less heat energy to eliminate polygalacturonase activity of the fruit.
                                                                                                                                                                                                                                                                      Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1996
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09-APR-1997
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                                                                                                                                               Conservative
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(first entry)
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                                                                                                                                                                        96.0%; Score 48; DB 2; 100.0%; Pred. No. 0.1;
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RESULT 4
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ID AAB4

AAB48353 standard; peptide; 10 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an internal fragment of the tomato CC polygalacturonase beta-subunit. The specification describes a CC polygalacturonase beta-subunit promoter. The promoter exhibits both high CC expression and high specificity, and provides tissue-preferential and CC developmentally regulated expression. The beta-subunit promoter is highly CC active in developing tomato fruit from as early as 10 days after CC pollination upto the onset of ripening, at which time it becomes CC inactive. The fruit specific, developmentally regulated promoter, can CC control the expression of target genes which affect the quality of CC developing fruit without affecting the ripening process. Target genes include genes responsible for sugar or starch metabolism, source sink CC relation, organic acid balance, flavour components, bathogen resistance, CC soluble solids, and water/pH relations. All or part of the promoter may be used to direct the expression of foreign or endogenous genes in the component of the promoter of the promoter may consider the expression of interest promoter in the constant of the promoter may be used to direct the expression of foreign or endogenous genes in the constant of the promoter may be used to direct the expression of foreign or endogenous genes in the constant of the promoter may be used to direct the expression of foreign or endogenous genes in the constant of the promoter may be used to direct the expression of foreign or endogenous genes in the constant of the promoter may be used to direct the expression of foreign or endogenous genes in the constant of the promoter may be used to direct the expression of foreign or endogenous genes in the constant of the promoter may be used to direct the expression of foreign or endogenous genes in the constant of the promoter may be used to direct the expression of the promoter may be used to direct the expression of the promoter may be used to direct the expression of the promoter may be used to direct the expression of the promoter may be us
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomato polygalacturonase beta-subunit promoter, useful for controlling expression of target genes which affect the quality of developing fruit without affecting the ripening process.
                                                                                                                                                                                                                                                                                                                       Sequence 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Col 9; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-611059/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dellapenna D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polygalacturonase beta-subunit; promoter; tomato; fruit; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polygalacturonase beta-subunit peptide produced after Lys-C digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB19329 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DELL/) DELLAPENNA D. (WATS/) WATSON C F.
                                                                                                                                                                                             Local
                                                                                                                                                           l Similarity 100 10; Conservative
                                                                       1 NGNGANGOXV 10
NGNGANGQXV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-00632806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-00632806
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                                                                                                                                                       96.0%; Score 48; DB
100.0%; Pred. No. 0.
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF;
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ABP35664
ID ABP3
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AC ABP2
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AC ABP2
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DX
CA----
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DB Fung
XX
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Seco
KW ant:
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                                                                                                                                                                                      RESULT 5
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                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a new method for modifying pectin that involves providing a host having pectin methylesterase (PME) activity and polygalacturonase (PG) activity, transforming the host by silencing PG activity to provide an increased PME to PG ratio, preparing a PME extract from the transformed host, and using the PME extract to modify pectin. A PME modified pectin is useful for foodstuffs preparation, and to impart an increased functionality to food products such as yogurt, milk/fruit juice and whey drinks. PME is useful to reduce the number of ester groups in a pectin in a block-wise manner, and to de-esterify two or more adjacent galacturonic acid residue of a pectin on at least substantially all of the pectin chains. The present sequence represents an internal peptide fragment of the PG enzyme, used for designing primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modifying pectin, for foodstuffs preparation, involves transforming host having pectin methylesterase (PME) and polygalacturonase (PG) activity by silencing PG activity, to increase PME to PG ratio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200078982-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Christensen TMIE, Kreiberg JD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polygalacturonase (PG) enzyme
Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine;
                                                                                                                                                                                                                                                                                                                                                           Sequence 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 42; 78pp; English.
                                                               Fungal
                                                                                             24-JUL-2002
                                                                                                                                                       ABP35664 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-091573/10.
                                                                ZBC
                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pectin methylesterase; PME; polygalacturonase; PG; tomato; pTOM6;
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                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                  NGNGANGQXV 10
                                                                                                                                                                                                                                       NGNGANGQXV
                                                             protein sequence #90.
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                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yogurt; milk; fruit juice; whey drink; de-esterification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99GB-00014209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                             entry)
                                                                                                                                                                                                                                                                                                              96.0%;
                                                                                                                                                         979
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                               Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internal Lys-C peptide fragment
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RESULT 6 AAB70839

AAB70839 standard; protein; 321 AA.

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S. halstedii

cellulase protein.

(revised)
(first entry)

Cellulase; fusion construct; protein synthesis; papermaking; glyceraldehyde phosphate dehydrogenase; food industry; feed washing composition; catalyst.

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                                                                                                                                                                                                                                                         cc antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as beta-lactam), an anti-hypercholesterolaemic (such as cyclosporin A), cc an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such as ovalicin), a glucan synthase inhibitor, glictoxxin family of compounds, cc a fungal toxin, a modulator of cell surface receptor signalling, a plant cc growth regulator, a pigment, an insecticide, or an antineoplastic cc compound. The method results in a decrease in fermentor run-time, a cc decrease in the size of the fermentor required for the production of cequivalent amounts of the secondary metabolite, or a decrease in the broadcation of cequivalent amounts of the production, which translates into decreased composes required for the production, which translates into decreased composes required for the production, which translates into decreased composes required for the production, which translates into decreased composes required for the production of the production of the production of the production of the production of the production of the production, which translates into decreased composes required for the production of the production of the production, which translates into decreased composes that must be handled in downstream processing. The sequences composed to the production of the printed specification, but the sequence composed to the production of the printed specification, but the sequence of the printed specification of the printed specification, but the sequences to the production of the printed specification, but the sequences to the production of the printed specification of the printed specification, but the sequences to the production of the printed specification of the printed sp
                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolite by a fungus. This involves modulating the expression of at least one ZBC (zinc binuclear cluster protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation the expression of at least one zinc binuclear cluster protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-2001; 2001WO-US029288
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                                                                                                                                                                                                                   Sequence 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 192; 49pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-352005/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to improving the production of a secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIA INC.
190 NGNGANG 196
                                                    1 NGNGANG 7
                                                                                                        Similarity 7; Conserv
                                                                                                           Conservative
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                                                                                               80.0%; 5c
100.0%; Pr
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                                                                                                                                        Score 40;
Pred. No.
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                                                                                                                 Mismatches
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                                                                                                                                        DB 5; L
                                                                                                                                                               Length 979;
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RESULT 7
AAW19210
ID AAW1
XX AAW1
AC AAW1
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DT 25-W
DT 29-S
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DE Cell
XX
KW Endc
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OS Cel:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CC This invention describes a novel microorganism (A) of the genus Ashbya CC for biotechnical production of proteins (I), containing a genetic CC construct so that the protein-synthesis capacity is altered relative to CC the wild-type species A gossypii ATCC 10895. The invention also CC from Streptomyces halstedii; (2) promoter (P) and transcriptional CC terminator (TT) from the sequence encoding the glyceraldehyde phosphate CC regulatory regions that provide expression in Ashbya; (4) a vector CC containing (IIa), p and/or TT, or the structure of (3), plus signals that CC provide replication in host cells or integration into a cellular genome; CC is transformed Ashbya, for production of cellulase, containing the CC structure of (3) in replicable form; (6) producing (I) using (A); (7) CC producing (A) by exchanging the promoter and/or increasing the gene copy commber, and/or by introducing a cellulase-encoding gene; and (B) (I) croduced by the method of (6). (A) are used for recombinant production of endogenous or exogenous proteins, specifically cellulase, useful in papermaking, medicine, food/feed industries, washing compositions and/or cas catalysts. (A) provide higher protein yields than wild-type cells. CC in the construction of the A. gossypii/S. halstedii genetic construct used to illustrate the method of the invention. (Updated on 06-AUG-2003 CC correct OS field.)
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 6
                                Endoglucanase; cenA gene; cellulase; cellulose; glucose
                                                                 Cellulomonas fimi endoglucanase
                                                                                                     25-MAR-2003
29-SEP-1997
                                                                                                                                                       AAW18210;
                                                                                                                                                                                AAW18210 standard; protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified Ashbya organisms with altered protein production properties, useful particularly for production of Streptomyces halstedii cellulas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF61508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Althoefer H, Pompejus M, Benito R, Santamaria R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces halstedii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    correct OS field.)
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                                                                                                                                                                                                                                                                   256 NGNGSNGE 263
                                                                                                                                                                                                                                                                                                  1 NGNGANGO 8
                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                 (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                    78.0%;
75.0%;
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Fernandez
                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                 Score 39; DB 4;
Pred. No. 1.2e+02;
2; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                Length 321;
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                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                             RESULT 8
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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18-DEC-1990;
19-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                The amino acid sequence (AAW18210) of a Cellulomonas fimi endo-1,4- beta-glucanase (EC-3.2.1.4) was deduced from an isolated DNA fragment (AAT71711) contg. the cenA gene. The enzyme is capable of hydrolysing beta-1,4-glycosidic linkages in the interior of a cellulose molecule, converting the cellulose to glucose. The C-terminal region of the enzyme is crucial for activity; deletion of 12 amino acids from that end results in loss of all activity. Recombinant endoglucanase can be expressed in host cells, esp. E. coli, utilising vectors incorporating the cenA gene. (Updated on 25-MAR-2003 to correct PF field.)
23-MAR-2001; 2001WO-US009231.
                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                               WO200171042-A2
                                                                      Drosophila melanogaster
                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 9876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloned Cellulomonas fimi cenA gene - conversion of cellulose to glucose.
                                                                                              pharmaceutical
                                                                                                                                                          26-MAR-2002
                                                                                                                                                                               ABB61028;
                                                                                                                                                                                                    ABB61028 standard; protein; 427
                                                                                                                                                                                                                                                                                                                                                            Sequence 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5A-F; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-350249/32.
N-PSDB; AAT71711.
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                381 NGNGSNGE 388
                                                                                                                                                                                                                                                                                      1 NGNGANGO 8
                                                                                                                                                                                                                                                                                                              Similarity
6; Conser
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller RC,
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86US-00894326.
90US-00630396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00185303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143. .165 // note= "Pro-Thr-rich conserved sequence of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .449
                                                                                                                                                                                                                                                                                                                        78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Warren
                                                                                                                                                                                                                                                                                                             Score 39; DB 2;
Pred. No. 1.7e+02;
2; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                   Length 449;
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Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 9876; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                   Maize MLO5 protein.
                                                                                                                                                                                                                                                                                                                            07-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable
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                                   07-JUL-1998;
                                                         07-JUL-1999;
                                                                                 13-JAN-2000
                                                                                                        WO200001722-A1.
                                                                                                                                                                   Domain
                                                                                                                                                                                                                              Zea mays.
                                                                                                                                                                                                                                                                 disease resistance;
                                                                                                                                                                                                                                                                           MLO5 protein; ZmMLO5; chromosome 3; mutation; recessive allele;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY.
             (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ention relates to an isolated nucleic acid detection of detecting 1000 or more genes from Drosophila. The
                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNGANGNHV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                   istance; pathogen; anti-infective; antipathogenic; antiviral;
antihelminthic; anti-arthropod; malze; HvMLO1.
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                                   98US-0091875P
                                                         99WO-US015255
                                                                                                                             /label= Transmembrane_helix 62. .149
/label= C-terminal_region
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70.0%;
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the maize MLO5 (ZmMLO5) protein, which exhibits sequence homology to barley MLO1 (HyMLO1) sequence. MLO5 protein is encoded by a mutation-induced recessive allele MLO5, located on chromosome 3, that confers resistance to plant pathogens. Expression of native MLO genes in plants can be altered by transforming them with a DN construct comprising the mutated MLO gene. Decreasing the expression or activity of native MLO protein leads to enhanced resistance of plants against pathogens such as fungi, virus, nematodes and insects. MLO gene can be used to isolate related sequences from other plants and as molecular markers used in breeding programs aimed at improving disease resistance. MLO protein has anti-infective, antipathogenic, antiviral, antifungal, antihelminthic and anti-arthropod activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 149 AA;
                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                    Venter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental
                                                                                                                                                                                                                                                                                                                                                                     (PEKE )
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                                                                                                                                                                                                                                                                                                                    JC,
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                                                                                                                                                                                                                                                                                                                                                                        CORP
                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                        NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 443
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85.7%;
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                                                                                                                                                                                                                                                                                                                       PWD,
                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biology;
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Pred. No. 1.2e
1; Mismatches
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The invention relates to an isolat capable of detecting 1000 or more

isolated nucleic r more genes from

acid detection reagent Drosophila. The invent

invention

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Disclosure; SEQ ID NO 10272; 21pp + Sequence Listing; English.

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RESULT 11
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ID ADA07853
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Matches 6
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Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                          Sequence 568 AA;
                                                                                                                                                                                                                                                                             The invention relates to an isolated polynucleotide that encodes nacrein. The methods and compositions of the present invention are useful for pearl oyster cultivation and pearl formation. The present sequence represents the amino acid sequence of Pinctada maxima nacrein.
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 24-25; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and polypeptide from the nacre gene of the Pinctada margaritifera species, useful for pearl oyster cultivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang FF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001; 2001US-0310070P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pinctada maxima nacrein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHAN/) CHANG F F. (LIHH/) LI H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HSIE/) HSIEH-LI H M.
387
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                                                                                                       l Similarity
6; Conserv
                                                     1 NGNGANG 7
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NGNGSNG
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                                                                                                             Conservative
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                                                                                                                                     74.0%;
85.7%;
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                                                                                                          1;
                                                                                                                                     Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cultivation; pearl formation.
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Pred. No. 3.6e+02;
                                                                                                       Mismatches
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                                                                                                                                        4.7e+02
                                                                                                                                                               DB 6;
                                                                                                          0;
                                                                                                                                                               Length 568;
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                                                                                                          Gaps
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RESULT 12

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ABB59482 standard; protein; 58
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ABB59482;
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26-MAR-2002 (first entry)
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26-MAR-2002 (first entry)
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26-MAR-2002 (first entry)
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Drosophila melanogaster.
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Drosophila melanogaster.
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Drosophila melanogaster.
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27-SEP-2001.
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PD
27-SEP-2001.
XX
23-MAR-2000; 2000US-0191637P.
PR
23-MAR-2000; 2000US-0191637P.
PR
11-JUL-2000; 2000US-0191637P.
PR
23-MAR-2000; 2000US-0191637P.
PR
23-MAR-2000; 2000US-0191637P.
PR
11-JUL-2000; 2000US-0191637P.
PR
23-MAR-2000; 000US-0191637P.
PR
23-MAR-200; 2000US-0191637P.
PR
23-MAR-200
RESULT 13
ABU15903
ID ABU15
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ABU15903
AC ABU15
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DT 19-JU
DT 19-JU
DX
DE Prote
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Antis
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                         Staphylococcus aureus
                                                                                                                      Antisense;
                                                                                                                                                                                Protein
                                                                                                                                                                                                                                       19-JUN-2003
                                                                                                                                                                                                                                                                                                 ABU15903;
                                                                                                                                                                                                                                                                                                                                                        ABU15903 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 5238; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                   prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                             by Prokaryotic
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                                                                                                                                                                                                                                                                                                                                                           1038
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Pred. No. 4.8e
1; Mismatches
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RESULT 14
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Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                        Sequence 1038 AA;
                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
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                                            ABB83327 standard; protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e invention relates to an isolated nucleic acid comprising any one of e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 43827; 1766pp; English.
                                                                                                                                                                                                                                     Conservative
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Carr GJ,
                                                                                                                                                                                                                                                        74.0%;
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Pred. No. 8.7e+02;
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Forsyth
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Xu HH;
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RESULT 15
ABR52643
ID ABR526
XX ABR527
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XX Multi
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XX Sacch
XX EP12!
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18-SEP-2001; 2001WO-FR002896.
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                                                                                                                                                                                                                                                                                                                                                   Multiprotein
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                                                   (CELL-) CELLZOME AG
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Search completed: July 21, 2004, 17:06:23 Job time: 5.07709 secs
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Best Local Similarity 85,,
Thes 6; Conservative
                                                                                                                                                                                                                                                              The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                Sequence 175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 151; 17pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, presently a drug target in the treatment or prevention of disease
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N-PSDB; ACC60685.
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       GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-286-691-27
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US-09-199-892-1
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US-08-273-538A-1 US-08-273-538A-1 IUS-08-273-538A-1 Sequence 1, Application US/08273538A Sequence 1, Application US/08273538A Patent No. 555831 GENERAL INFORMATION: APPLICANT: DellaPenna, Dean ITITE OF INVENTION: Altered Polygalacturonase Isoforms NOWHER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSEE: Nicholas J. Seay STREET: P.O. BOX 2113 CITY: Madison STATE: Wisconsin COUNTRY: USA ZIP: 5370-12113 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk MEDIUM TYPE: Ploppy disk MEDIUM TYPE: Ploppy disk MEDIUM TYPE: PLOPS/MS-DOS SOFTWARE: Microsoft Word COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOft Word COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOft Word COPERATION NUMBER: US/08/273,538A FILLNG DATE: APPLICATION NUMBER: US/08/273,538A FILLNG DATE: APPLICATION NUMBER: 2736 TELECOMUNICATION INFORMATION: NAME: Seay, NICHOLAS J REGISTRATION NUMBER: 2736 TELECOMUNICATION INFORMATION: TELESPAX: 608/251-5000 TELESPAX: 608/251-9166 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LERGINAL SOURCE: TYPE: amino acid TOPOLOGY: Linear MOLECULE TYPE: peptide HYPOTHETICAL: NO TRACKINAL SOURCE: ORGANISM: Lycopersicon esculentum US-08-273-538A-1  Query Match Sest Jocal Similarity 100.0%; Pred. No. 0.041;	ALIGNMENTS	28 34 68.0 211 1 US-08-899-575-34 Sequence 34, Appl 30 34 68.0 211 1 US-08-899-575-34 Sequence 34, Appl 30 34 68.0 211 2 US-08-383-619-16 Sequence 16, Appl 31 34 68.0 211 3 US-08-997-739-16 Sequence 16, Appl 32 34 68.0 211 3 US-08-997-739-16 Sequence 16, Appl 33 34 68.0 211 5 PCT-US93-08364-16 Sequence 16, Appl 34 68.0 231 5 PCT-US93-08364-16 Sequence 16, Appl 35 34 68.0 231 5 PCT-US93-08364-16 Sequence 16, Appl 36 34 68.0 232 2 US-08-829-876-103 Sequence 103, Appl 37 34 68.0 232 4 US-09-234-873A-103 Sequence 103, Appl 38 34 68.0 232 2 US-08-829-876-101 Sequence 103, Appl 39 34 68.0 233 2 US-08-829-876-105 Sequence 101, Appl 39 34 68.0 233 3 US-08-438-745-17 Sequence 105, Appl 40 34 68.0 233 3 US-08-438-745-17 Sequence 105, Appl 41 34 68.0 233 3 US-09-219-019-15 Sequence 17, Appl 44 34 68.0 233 3 US-09-219-019-15 Sequence 17, Appl 44 34 68.0 233 4 US-09-234-874A-105 Sequence 17, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 17, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105, Appl 45 34 68.0 233 4 US-09-234-874A-105 Sequence 105,
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US-08-632-806A-1

Sequence 1, Application US/08632806A Patent No. 6127179

Patent No.

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US-09-286-691-27
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                                                                                                                                           Sequence 27, Application US/09286691
Patent No. 6190189
GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Cellulases and Coding
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       PILE REFERENCE: 42-96
CURRENT APPLICATION NUMBER: US/09/286,691
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,883
EARLIER FILING DATE: 1996-10-04
EARLIER APPLICATION NUMBER: PCT US97/18008
EARLIER FILING DATE: 1997-10-03
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FRAGMENT TYPE: interna ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/632,806A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DellaPenna, Dean
APPLICANT: Watson, Colin F.
TITLE OF INVENTION: Gene Promoter for Tomato Fruit
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1
STREET: 1
STREET: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 53703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Quartes a street STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 10; 0.041;
                                                                                                                                                 Sequences
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Query Match
Best Local Similarity
Fatches 6; Conserve
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                              ; FEATURE:
; OTHER INFORMATION: Mlo5
US-09-347-650-8
                                                                                                                                                                                                                                                                                                            US-09-347-650-8
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CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/027,883
PRIOR FILING DATE: 1996-10-04
PRIOR PPLICATION NUMBER: PCT US97/18008
PRIOR FILING DATE: 1997-10-03
PRIOR APPLICATION NUMBER: 09/286,691
PRIOR APPLICATION NUMBER: 09/286,691
PRIOR FILING DATE: 1999-04-05
                                                                                                                    FILE REFERENCE: 5718-42035718/158714
CURRENT APPLICATION NUMBER: US/09/347,650
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Briggs, Steven
TITLE OF INVENTION: in Plants
TITLE OF INVENTION: in Plants
                                                                                                                                                                                                                                                                           Sequence 8, Application US/09347650 Patent No. 6576814
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Patent No. 6268198
 Query Match
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                                                                       LENGTH: 149
TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Cellulomonas fimi
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nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                     218 NGNGSNGE 225
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Chen, Huizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, Xin-Liang
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75.0%;
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75.0%;
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 74.0%;
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Pred. No. 38;
2; Mismatches
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   Score 37;
   DB 4;
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Length 149;
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RESULT 6
US-08-811-492-127
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                                                                                                                                                                                                                                                     CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,885

FILING DATE: 03-NOV-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139

FILING DATE: 09-DEC-1992

CLASSIFICATION: 435
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                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-927-5054
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC\ DOS/MS\ DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MODIFIED PROTEINS, METHODS TITLE OF INVENTION: PRODUCTION AND METHODS FOR TITLE OF INVENTION: PROTEINS
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STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 29-DEC CLASSIFICATION: 435
                                                                                                                                  TELEFAX: 509-927-1705
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CLASSIFICATION: 435
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STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                             amino acids
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                   3S: single
linear
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                                                                                                    127:
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1; Mismatches
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PURIFICATION OF TARGET
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RESULT 8
US-09-199-892-1
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                                                                                                                                                                           US-08-773-910-1
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                                                                                                                 Matches
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Best Local Similarity 85.7%;
                                                                                                                                Best
                                                                                                                                            Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: GenBau
CLONE: 1715374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,910
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                         70.0%;
Local Similarity 85.7%;
hes 6; Conservative
                                                                                                                                                                                                                             TYPE: STRANDEDNESS: SIL
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                          LENGTH:
                                                            49
                                                                                       1 NGNGANG 7
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1715374
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                                                            NGNGKNG 55
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                                                                                                                                Score 35; DB 2;
Pred. No. 1.3e+02;
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                                                                                                                   Mismatches
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                                                                                                                                             Length 232;
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                                                                                                                   Gaps
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Sequence 1, Application US/09199892 Patent No. 6307021

GENERAL INFORMATION:

⊳anαman, Olga Goli, Surya K. Hill™~-

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Query Match
Best Local Similarity
Watches 6; Conserve
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US-09-240-639-10
                                                  FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 455
                                                                                                                                                                                 Sequence 10, Application US/09240639

Patent No. 6350447

Patent No. 6350447

Patent INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maxia
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 232 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                 TYPE: PRT ORGANISM: P. sativum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1715374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN APOPTOSIS REG
TITLE OF INVENTION: ULATOR
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Por CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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Pred. No. 1.3e+02;
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GENERAL INFORMATION:
                                                             Matches
                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 574 amino acid res
                                                                                                                                                                                                                               MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 98-0989*/LC(WMC)/144
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: September 10, 1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                             NAME/KEY:
LOCATION:
                                                     70.0%;
Local Similarity 85.7%;
les 6; Conservative
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CITY: Washington
STATE: D.C.
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                 IDENTIFICATION METHOD:
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71 NGNGASG
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                                1 NGNGANG 7
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                                                                                                                                                                                                                                                                                                             574 amino acid residues
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No. 6337201 relevant
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KOJÍ YANAI et al.

JENTION: -FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
JENTION: ISOLATING -FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCING
JENTION: -FRUCTOFURANOSIDASE, AND -FRUCTOFURANOSIDASE VARIANT
                                                                                                                                                                 mat peptide
1 .. 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible SYSTEM: MS-DOS
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                                                                                                                                                                                                               Scopulariopsis brevicaulis IFO4843
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                                                               Score 35; DB 4; Length 574; Pred. No. 3.4e+02; 1; Mismatches 0; Indels
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Pred. No. 2.7e+02;
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RESULT 11 US-09-508-264A-3 ; Sequence 3, Application US/09508264A ; Patent No. 6566111

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-28
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US-09-268-347-34
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/09268347
Patent No. 6335182
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
APPLICANT: LOOSMORE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-660
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 1104
                                                                                                                                                                                       Sequence 34, Application US/09268347 Patent No. 6335182
                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: KONO, Toshiaki
TITLE OF INVENTION: Beta-Fructofuranosidase
FILE REFERENCE: 2000-0267*/LC/00144
CURRENT APPLICATION NUMBER: US/09/508,264A
CURRENT FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: PCT/JP98/04087
PRIOR FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: YANAI, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP/245154/1997
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: mat peptide
LOCATION: (1)...(613)
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85.7%;
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85.7%;
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Pred. No.
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Pred. No. 3.7e+02;
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6.7e+02;
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5178861-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Haemophilus influenzae US-09-268-347-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-178-477B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; APPLICANT: VERGARA, ULISES;RUIZ, ANDRES;FERREIRA, ARTURO;
;NUSSENZWEIG, RUTH S.;NUSSENZWEIG, VICTOR N.
; TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF CIRCUMPOROZOITE PROTEINS NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5178861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08178477B
Patent No. 5756343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local 9
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Best Local
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WU, CARL; CLOS, JOACHIM;
APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN,
TITLE OF INVENTION: CELL STRESS
TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/37
FILING DATE: 22-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
            APPLICATION NUMBER: US/08/
FILING DATE: 07-JAN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/
FILING DATE: 26-NOV-1990
CLASSIFICATION: 530
                                                                                                                                                                                            ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
ATTORNEY/AGENT INFORMATION:
                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                  CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 6; Conserv
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Local Similarity 85.7%;
les 6; Conservative
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                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 11
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                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                     MORGAN & FINNEGAN
                                                                                                                                                                                                   FLOPPY DISK
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85.7%;
                                                                                                               US/08/178,477B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB Pred. No. 8.1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB Pred. No. 6.7e.
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NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4103US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 758-4800
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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50
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/ (gn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/ (gn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/ (gn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/ (gn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/ (gn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/ (gn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

1 1 1 1	atobe		тепдсп	Ħ	TD	Description
₽	40	80.0	451	15	US-10-369-493-4148	Sequence 4148, Ap
2	40	80.0	979	9	US-09-801-368-284	
ω	40	80.0	979	16	US-10-149-310-192	Sequence 192, App
4	37	74.0	187	12	US-10-425-114-53903	53903
υ	37	74.0	260	12	US-10-425-114-56925	56925
თ	37	74.0	380	12	US-10-425-114-44021	44021,
7	37	74.0	452	16	US-10-437-963-201301	
œ	37	74.0	482	12	US-10-424-599-150886	
Q	37	74.0	568	14	US-10-086-510-5	
10	37	74.0	1038	12	US-10-282-122A-43827	4.
11	36	72.0	296	10	US-09-949-029-70	70, Apr
12	36	72.0	376	12	US-10-425-114-44598	
٦ ا	36	72.0	420	14	US-10-032-585-7653	Sequence 7653, Ap
14	36	72.0	572	12	US-10-424-599-145867	
15	36	72.0	763	14	US-10-156-761-12117	Sequence 12117, A

RESULT 2

45	44	43	42	41	40	39	88	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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187	187	159	158	158	152	152	152	152	150	98	80	53	26	972	972	728	659	574	558	525	328	232	219	189	86	1018	1018	887	796
12	12	10	14	9	16	15	15	12	9	16	12	12	12	15	15	14	15			12	14	9	12	16	11	9	φ	12	15
- 1	US-10-399-883-34	726-258-	-234-671-	056-1	-437-963-	-674	045-674-	-306	84-767A-	0-437-963-12179	10-424-599-	4915	10-329-7812	-10-3	69-493-6	-032-585-75	US-10-369-493-1663	US-09-990-385-13	US-10-282-122A-50632	US-10-282-122A-64763	US-10-032-585-7434	US-09-957-295-1	US-10-170-385-217	US-10-437-963-170736	US-09-864-408A-7302	US-09-815-242-12838	US-09-815-242-5797	82-12	US-10-369-493-3508
416,	34,	53	e 131,	102	16948	Sequence 584, App	454,	e 197	Sequence 217, App	Sequence 121796,	Sequence 250266,	149155	1, Apr	Sequence 6222, Ap	6221,	7547,	e 1663,	13, Ap		Sequence 64763, A	Sequence 7434, Ap	Sequence 1, Appli	Sequence 217, App	Sequence 170736,	Sequence 7302, Ap	Sequence 12838, A	5797,	49386,	Sequence 3508, Ap

## ALIGNMENTS

```
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 4148

LENGTH: 451
  B
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                                                                                                                                                          US-10-369-493-4148
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US-10-369-493-4148
                                                                             Best Local
Matches
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                                                                                                                Query Match
                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(451
OTHER INFORMATION:
                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Neurospora crassa
FEATURE:
  277
                                     1 NGNGANGQ 8
                                                                           l Similarity
7; Conserv
NGNGASGQ 284
                                                                             Conservative
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87.5%;
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                                                                        Score 40; DB 15; 1
Pred. No. 1.1e+02;
1; Mismatches 0;
                                                                                                              Length 451;
                                                                           Indels
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US-09-801-368-284

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US-10-149-310-192

Sequence 192, Application US/10149310

Publication No. US20040077039A1

GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
APPLICANT: Maxon, Mary
APPLICANT: Maxon, Mary

FILLE OF INVENTION: Modulation of Secondary Metabolite Production by
TITLE OF INVENTION: Zinc Binuclear Cluster Proteins

FILE REFERENCE: 14184-019US1

CURRENT FILING DATE: 2001-02-19

PRIOR APPLICATION NUMBER: US/10/149,310

CURRENT FILING DATE: 2001-09-19

PRIOR APPLICATION NUMBER: PCT/US01/29288

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19
18
                                  Query Match
Best Local Similarity
Thes 7; Conserve
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                                                                                                                                        US-10-149-310-192
                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/233,564
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEQ ID NO 192
TLENGTH: 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
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                                                                                                                                                         TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 979
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Maxon, Mary
Milne, Todd
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Holtzman, Doug
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                                                       Conservative
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100.0%; Pred. No.
                                                                            100.0%;
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                                                                          Score 40; DB 16;
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SEQ ID NO 53903
LENGTH: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53903, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                             SEQ ID NO 56925
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Publication No. US20040034888A1
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Matches 6; Conserv
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                                                                                                             Query Match
                                                                                                                                                                                                                                                                                        APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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APPLICANT:
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                                                                                                                                                                    OTHER INFORMATION: Clone ID: UC-ZMFLM017086H05_FLI.pep
                                                                                                                                                                                                        ORGANISM: Zea mays
                                                                                                                                                                                        FEATURE:
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207 NGNGSNG 213
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                                   1 NGNGANG 7
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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Kovalic, David K
Screen, Steven E
                                                                          Conservative
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                                                                                            74.0%;
85.7%;
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85.7%;
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Pred. No. 2e+02;
1; Mismatches
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Pred. No. 1.5e+02;
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                                                                                                           DB 12; Length 260;
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RESULT 6

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RESULT 8
US-10-424-599-150886
; Sequence 150886, Application US/10424599
; Publication No. US20040031072A1
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Best Local Similarity
7; Conserve
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Best Local Similarity
Matches 6; Conserva
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US-10-425-114-44021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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LENGTH: 380
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
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APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221)B
                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                                                                                                            246 NGNGDHGQLV 255
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                                                                                                                                                                                   Conservative
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85.7%;
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Pred. No. 3.6e+02;
1; Mismatches 2
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RESULT 10
US-10-282-122A-43827
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                                                    GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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SEQ ID NO 150886
LENGTH: 482
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                Sequence 43827, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
LENGTH: 568
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/310,070
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 505493000120
CURRENT APPLICATION NUMBER: US/10/086,510
CURRENT FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fang-Tseh (Frank) CHANG et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEARL
TITLE OF INVENTION: OYSTER CULTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28
                    APPLICANT:
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APPLICANT: Cao Yongwei
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APPLICANT: Kovalic David
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LOCATION: (1)..(482)
OTHER_INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: Clone ID:
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Local Similarity 85.7%;
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Local Similarity 85.7%;
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                  Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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                                                                                                                                                                                                                                                                                                                                                Score 37; DB 14; Length 568; Pred. No. 4.5e+02;
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Wall, Daniel

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GENERAL INFORMATION:
APPLICANT: Karpen, G.H.
APPLICANT: Dobie, K.W.
APPLICANT: Kennedy, C.D.
APPLICANT: Velasco, V.M.
APPLICANT: McGrath, T.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-282-122A-43827
                                                   APPLICANT: Patterson, R.W.

APPLICANT: Patterson, R.W.

TITLE OF INVENTION: Identification of chromosome inheritance modifiers in Drosophila TITLE OF INVENTION: melanogaster

FILE REFERENCE: 121.015US1

CURRENT APPLICATION NUMBER: US/09/949,029

CURRENT FILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: US 60/231,178

PRIOR FILING DATE: 2000-09-07

NUMBER OF SEQ ID NOS: 149

SOFTWARE: FeatSEQ for Windows Version 4.0

SEQ ID NO 70

SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
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Best Local :
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-02-09
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LENGTH: 296
TYPE: PRT
ORGANISM: Drosophila melanogaster
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APPLICATION NUMBER: 60/230,347
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APPLICATION NUMBER: 60/242,578
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US-10-032-585-7653
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                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7653
                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US20 GENERAL INFORMATION:
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SEQ ID NO 44598
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Matches 6; Conserv
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Matches 6; Conserv
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                    APPLICANT: Terry, Roemer D.
APPLICANT: Bo, diang
APPLICANT: Bo, diang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 10182-005-999
                                                                                                                                                      LENGTH: 420
TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 376
TYPE: PRT
ORGANISM: Glycine
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 189 NGGGANGE 196
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75.0%;
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Pred. No. 3.4e+02;
0; Mismatches 1
                                                                      1; Mismatches
                                                                                   Score 36; DB 14;
Pred. No. 4.8e+02;
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Pred. No. 4.3e+02;
1; Mismatches 1
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12117
LENGTH: 763
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US-10-156-761-12117
; Sequence 12117, Application US/10156761
; Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-12117
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_102737C.1.pep
US-10-424-599-145867
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US-10-424-599-145867
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5322)B
FILE REPERENCE: 38-21(5322)B
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FILE REPERENCE: 38-21(5
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                               Matches
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)...(572)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
FEATURE:
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Local Similarity 85.7%;
les 6; Conservation
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744 NGNGGNG 750
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Search completed: July 21, 2004, 17:17:49 Job time: 2.73448 secs

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Result
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Maximum Match 100
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 protein search, using sw model
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length: 2000000000
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histone H1.4 - Cae
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protein C18G1.5 [i
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424	362	341	245	213	1279	1043	1018	972	969	830	601	570	525	510	455
Д	N			N				N	2	N	N	N	N	N	2
Z3BPFD	G84526	G64058	F70787	G82723	T18312	AH1906	T22318	T22488	F71418	S54547	C89451	T49181	D70878	T22835	S48859
coat protein A pre	hypothetical prote	UDP-N-acetylmurama	hypothetical glyci	partition protein	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	PAM1 protein - yea	protein T04G9.6 [i	cyclophylin-like p	hypothetical glyci	hypothetical prote	nucleoside triphos

## ALIGNMENTS

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A;Molecule type: protein
A;Residues: 109-119;160-171;230-236;243-251;291-293 <ZHE1>
A;Residues: 109-119;160-171;230-236;243-251;291-293 <ZHE1>
A;Residues: 109-119;160-171;230-236;243-251;291-293 <ZHE1>
A;Resperimental source: fruit, cv. Ailsa Craig
C;Comment: This enzyme is a cell wall protein that hydrolyzes pectins.
C;Keywords: cell wall; glycoprotein; glycosidase; hydrolase; polysaccharide degradation F;1-30/Domain: signal sequence #status predicted <FRO>
F;1-109/Domain: amino-terminal propeptide #status predicted <MAT>
F;109-387/Product: polygalacturonase 1 beta chain #status experimental <MAT>
F;398-30/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;124,142,256,334,369,387/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                               R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A,Title: Complete genome sequence of Treponema pallidum, the syphilis A;Reference number: A71250; MUID:98332770; PMID:965876
A;Accession: D71260
A;Status: preliminary; nucleic acid sequence not shown; translation namelecule type. Name
                                                        A; Molecule type: DNA
A; Residues: 1-539 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein TP0969 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: D71260
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A; Residues: 1-630 < ZHE>
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A;Accession: JQ1670
A;Accession: JQ1670
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A;Title: The beta subunit of tomato fru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polygalacturonase (EC 3.2.1.15) 1 beta chain precursor - tomato C;Species: Lycopersicon esculentum (tomato) C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 21-Jul-2000 C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 21-Jul-2000 C;Date: Total Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | P
A;Cross-references: GB:AE001264; GB:AE000520; NID:g3323278; PIDN:AAC65927.1; PID:g332329
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8; Conserv
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Pred. No. 1.8;
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M.; Utterback,
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C;Genetics:
A;Gene: SPAC30D11.14
A;Map position: 1L
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S62572
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A;Gene: TP0969
                                                                                                                   A;Cross-references: EMBL:X74152; NID:g450363; PIDN:CAA52267.1; A;Experimental source: strain S288C R;Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: protein YKL015w
C;Species: Saccharomyces cervisiae
C;Date: 07-Feb-1992 #sequence revision 07-Feb-1992 #text_change
C;Accession: A39792; S34701; S37828; S37832; S16705
A; Cross-references:
A; Experimental source
                                                                                A; Reference number: S37825
A; Accession: S37828
                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-979 <WIE>
                                                                                                                                                                                                                                            A,Description: Sequencing and analysis of 51.5 kilobases on A,Reference number: S34679
A,Accession: S34701
                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:X55384; NID:g4251; PIDN:CAA39055.1; PID:g4252 R;Wieman, S.; Voss, H.; Schwagaer, C.; Rupp, T.; Stegemann, J.; Zimmu submitted to the EMBL Data Library, July 1993
                                                                                                                                                                                                                                                                                                                                                                                                                           R;Marczak, J.E.; Brandriss, M.C.
Mol. Cell. Biol. 11, 2609-2619, 1991
A;Title: Analysis of constitutive and noninducible mutations
A;Reference number: A39792; MUID:91203881; PMID:2017167
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A; Accession: T38585
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                                        A;Residues: 1-979 <WI2>
                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-979 <MAR>
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                                                           A; Molecule type: DNA
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8; Conser
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  EMBL:Z28015; NID:g486002; ce: strain S288C
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                       PIDN: CAA81850.1;
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                  PID:g486003; MIPS:YKL015w
                                                                                                                                               Sensen, C.;
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comp.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70811
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S.
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F;34-60/Region: zinc finger
                                                                                                                 Gene 44, 315-324, 1986
A; Title: Characterization and structure of A; Reference number: A24993; MUID:87055249;
                                                                                                                                                                                                                                                                                                                           RESULT
A24993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-137 < COL>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical glycine-rich protein Rv0832 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Rieger, M.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37832
A;Accession: S37832
A; Molecule type: DNA
A; Residues: 1-449 <WON>
A; Cross-references: GB:M15823; NID:g144409; PIDN:AAA23084.1; PID:g144410
A; Note: the amino-terminal sequence of the mature protein (residues 32-62)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain C; Genetics:
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A; Residues: 1-825 < RIE>
                                                                                              A; Accession: A24993
                                                                                                                                                                                      R; Wong, W.K.R.; Gerhard, B.; Guo,
                                                                                                                                                                                                              C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Mar-2000
C;Accession: A24993
                                                                                                                                                                                                                                                      C; Species: Cellulomonas fimi
                                                                                                                                                                                                                                                                              N; Alternate names: endo-1,
                                                                                                                                                                                                                                                                                                 cellulase (EC 3.2.1.4) precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD:S0001498; MIPS:YKL015w
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Pred. No.
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Pred. No.
                                                                                                                                                                                      Z.M.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr.,
                                                                                                                                                                                                                                                                                                           Cellulomonas
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C; Date: 1. 202353
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R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Xuritz, T.; Sasamoto, S.; Maranawo, T.; Nakamura, Y.; Wolk, C.P.; Xuritz, T.; Sasamoto, S.; Maranawo, M.; Tabata, S.; R; Kaneko, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Tabata, S. Nakazaki, N.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Ya
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A; Gene: cenA
C; Function:
                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-694 <XUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation elongation factor EF-G [imported] - Nostoc sp. (straC;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: This protein is rich in asparagine and glycine residues, ayers. It is also important in calcification. C;Keywords: matrix protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kono, M.; Hayashi, N.; Samata, T.
Biochem. Biophys. Res. Commun. 269, 213-218, 2000
A;Title: Molecular mechanism of the nacreous layer formation
A;Reference number: JC7210; MUID:20160475; PMID:10694502
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A; Residues: 1-568 < KON>
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                                                                                                                                          Superfamily:
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6; Conserv
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                                                                                                                                        translation elongation factor
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85.7%;
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75.0%;
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C 7120
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Pred. No.
                                        Pred. No. 58;
l; Mismatches
                                                                                       Score 37;
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A; Residues: 1-1519 <OTO>
A; Cross-references: GB:L
A; Accession: $77974
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A;Title: Identification and
A;Reference number: $41525;
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C;Species: Helicobacter mustelae

C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997

C;Accession: S41525; S77974

R;O'Toole, P.W.; Austin, J.W.; Trust, T.J.

Mol. Microbiol. 11, 349-361, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession. A; Accession A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1038 < KUR>
A; Residues: 1-2038 < KUR>
A; Cross-references: GB: BA000018; PID: g13702453; PIDN: BAB43594.1; GSPDB: GN00149
A; Cross-reference: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kuroda, M.; Ohta, T.; Uchlyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimi C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H90053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major ring-forming surface protein precursor - Helicobacter
                                                                                                                                                                              ;1-47/Domain: signal sequence #status;48-1519/Product: major ring-forming s
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NGNGNNGAAV 895
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60.0%;
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70.0%;
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88;
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#text\_change

23-Mar-2001

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R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions A;Reference number: 220488; MUID:94088747; PMID:8264798
A;Accession: T28568
                                                                                                                                               A;Experimental source: strain Garcia-1966
C;Genetics:
                                                                                                                                                                                                                                                                 R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49071.1; PID:g457021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Blinov, V.M.
submitted to GenBank, November
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                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-101 <SHC>
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C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
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                                                                              Query Match
Best Local
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Pred. No. 7.9;
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Pred. No.
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RESULT 14

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R;anonymous, The C. elegans Sequencing Consortium.

R;anonymous, The C. elegans Sequencing Consortium.

R;anonymous, The C. elegans Sequence 282, 2012-2018, 1998

A;Cience 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/A;Note: published_errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49918.1; R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YBR254c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1772
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: S32957; S46135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein C18G1.5 (imported) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.
Yeast 9, 189-199, 1993
A;Title: The complete sequence of a 19,482 bp segment located
A;Reference number: S29348; MUID:93220397; PMID:8465606
Search completed: July 21, Job time : 1.6424 secs
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C; Superfamily: histone
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A; Residues: 1-253 < STO>
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A; Residues: 1-175 < AIG>
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A;Accession: S46135
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Best Local
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Map position: 2R
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 5:
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ota; Schizosaccharomycetes;
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PIR; A39792; A39792.
PDB; 1AJY; 17-SEP-97.
PDB; 1ZME; 16-SEP-98.
GO; GO:0005634; C:nucleus; IC.
GO; GO:0003704; F:specific RNA polymerase II transcription fa.
GO; GO:0045944; P:positive regulation of transcription from P.
GO; GO:0006562; P:proline catabolism; IMP.
InterPro; IPR007219; Fungal_trans.
InterPro; IPR001138; Fungi_TrN.
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MEDLINE=97448679; PubMed=9303004;

Swaminathan K., Flynn P., Reece R.J., Marmorstein R.;

"Crystal structure of a PUT3-DNA complex reveals a novel mechanical structure of a protein containing a Zn2Cys6 binuclear
                                                                                                                        GermOnline;
                                                                                                                                                                                                                                         or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walters K.J., Dayie K.T., Reece R.J., Ptas "Structure and mobility of the PUT3 dimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97448678; PubMed=9303003;
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Yeast 9:1343-1348(1993).
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"Analysis of constitutive and noninducible mutations transcriptional activator.";
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othues D., Sensen C.,
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Endoglucanase 1 precursor (BC 3.2.1.4) (Endo-1,4-beta-glucanase (CEL) (CEL)).
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Fernandez-Abalos J.M., Sanchez P., Coll-Fr
Villanueva J.R., Perez P., Santamaria R.I.
"Cloning and nucleotide sequence of celA1,
endo-beta-1,4-glucanase-encoding gene from
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                                                                                                                                                                                                                                                          Gilkes N.R., Claeyssens M., Aebersold R., Henrissat B., Morrison H.D., Kilburn D.G., Warren R.A.J., Miller R.C. "Structural and functional relationships in two families
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87055249; PubMed=3023193; MEDLINE=87055249; PubMed=3023193; MEDLINE=8705249; PubMed=3023193;
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PROSITE; PS00655; GLYCOSYL_HYDROL_F6_2;
PROSITE; PS00656; GLYCOSYL_HYDROL_F6_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001524; Glyco_hydro_
Pfam; PF01341; Glyco_hydro_6; 1.
PRINTS; PR00733; GLHYDRLASE6.
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90036847; PubMed=2681184; Gilkes N.R., Kilburn D.G., Miller R. "Structural and functional analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization and structure Cellulomonas fimi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wong W.K.R.,
Miller R.C.
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HSSP; P26222; 1TML.
                                                                                                                                                                                                                                  glycanases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria;
Micrococcineae; Cellulomor
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                                                                                                                                                                                                                                                                                                                                               DISULFIDE BONDS.
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                                                                                                                                                                                                                                                        "Structural and functional relationships
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                                                                                                                                                                                                                                                                                                                                                                                      Biol.
               PUNCTION: The biological conversion of cellulose to glucose generally requires three types of hydrolytic enzymes: (1) Endoglucanases which cut internal beta-1,4-glucosidic bonds; Exocellobiohydrolases that cut the dissaccharide cellobiose from the nonreducing end of the cellulose polymer chain; (3) Beta-1,4-glucosidases which hydrolyze the cellobiose and oth short cello-oligosaccharides to glucose CARTAITIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and gereal beta-D-glucosis.
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1 27
28 321 ENDOGLUCANASE 1.
110 110 BY SIMILARITY.
119 149 PROTON DONOR (BY S
295 295 NUCLEOPHILE (BY SI
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linker region
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BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
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5.9;
  cereal beta-D-glucans. "hinge") may be a pote
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cellulase
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site for proteolysis.
SIMILARITY: Belongs to cellulase family B (family 6 of glycoshydrolases).
SIMILARITY: Contains 1 bacterial-type cellulose-binding (CBD)

glycosyl

domain.

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RESULT 6
TR20 YEAST
ID TR20 Y
AC P38334
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 028-FEB
DE Transp
GN TRS20
OS Saccha
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Matches
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Pfam; pF00553; CBM_2; 1.

Pfam; pF00353; GLM_2; 1.

PFAM; pF00373; Glyco_hydro_6; 1.

PRINTS; pR00733; Glyco_hydro_6; 1.

PROBITE; p500637; CBD_II; 1.

PROSITE; pS00561; CBD_BACTERIAL; 1.

PROSITE; pS00565; GLYCOSYL_HYDROL_F6_2; 1.

R PROSITE; pS00656; GLYCOSYL_HYDROL_F6_2; 1.

R PROSITE; pS00656; GLYCOSYL_HYDROL_F6_2; 1.
                                                                                                                                                                                                                                                                                                                                                                      Query Match
 "The complete sequence of a 19,482 bp segment arm of chromosome II from Saccharomyces cerev Yeast 9:189-199(1993).
                                                                                                                                                           TR20_YEAST STANDARD; PRT; 175 AA. p38334; 01-OCT-1994 (Rel. 30, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Transport protein particle 20 kDa subunit (TRAPP 20 TRS20 OR YBR254C OR YBR1722.
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ACT_SITE
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DISULFID
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DISULFID
                                                                            STRAIN=S288c;
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                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                               TaxID=4932;
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Cellul_bind.
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CELLUICOSE-BINDING.
LINKER ("HINGE") (PRO-THR BOX)
CATALYTIC.
BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                     Score 39;
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                                      segment located
                          cerevisiae.";
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01-JUL-1989
01-JUL-1989
10-OCT-2003
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Prilipov A.G., Selivanov N.A., Efimov V.P., Marusich
Mesyanzhinov V.V.;
"Nucleotide sequences of bacteriophage T4 genes 9, 10
"Nucleic Acids Res. 17:3303-3303 (1989).
                                                                                                        Miller E.S., Kutter E., Mosig G., "Bacteriophage T4 genome."; Microbiol. Mol. Biol. Rev. 67:86-
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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) MEDLINE=20015372; PubMed=10545330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, T4-like viruses.
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SGD; S0000458; TRS20.
GO; GO:0003008; CITRAPP; IDA.
GO; GO:0006888; P:ER to Golgi transport; IMP.
INTERPRO; IPRO06732; Sedlin N.
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EMBL; Z36123; CAA85217.1;
PIR; S32957; S32957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   MEDLINE=22514363; PubMed=12626685;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baseplate structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VG09_BPT4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: TRAPP plays a key role in the late stages of endoplasmic
reticulum to Golgi traffic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
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85.7%;
                                                                                                               Rev. 67:86-156(2003).
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Pred. No.
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                                                                                                                                                                              Arisaka F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288
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                                                                                                                                                                              Kunisawa
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                                                                                                                                                                              Τ.,
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                                                                                                                                                                              Ruger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tail contraction."
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                                                                                                                                                                                                                                                                                                                                                                Structural
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                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Structural component of the baseplate. Connects the long tail fibers to the baseplate and triggers the tail contraction after virus attachment to a host cell.
                                                                                                                                                                                                                                                                                                                                                                              S04082; GNBPT4.
LOEX; 05-OCT-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                              AF158101; AAD42520.1; -.
52
               μ
                             . Similarity 6; Conserv
NGTGADGQII 61
               NGNGANGOXV 10
                                                                                                                                                                                                                                                                                                                                                                       IPR008987; Gp9
                                                                                                                                                                                                                                                                                                                                                                protein;
                                                              288
                               Conservative
                                                              AA;
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180
193
193
193
196
208
210
2224
2224
255
255
266
                                                                                                                                                                                                          282
30997 MW;
                                                                                                                                                                                                                                                                                                                                                                 3D-structure
                                      72.0%;
                                     Score 36; DB
Pred. No. 18;
                                                              8028FCEBA25BB760 CRC64;
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                              DB 1;
                                              Length 288;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strelkov S.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL
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RESULT 8
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Q9XA16;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-2196410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kleser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL939118; CAB45215.1; -.
plr; T36717; T36717.
InterPro; IPR005243; PASTA.
InterPro; IPR0007719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hopwood D.A.; (Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147(2002).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycineae; Streptomycetaceae; NCBI_TaxID=1902; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOXA16;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation kinase SCO3848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03793; PASTA; 4.
Pfam; PF00009; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00740; PASTA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable serine/threonine-protein SCO3848 OR SCH69.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50011; PROTEIN_KINASE_DOM PROSITE; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_
PROSITE; PS50011; PROTEIN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the Ser/Thr fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
  654
                                                                                       Similarity 6; Conserv
  NGNGGNG
                                             NGNGANG 7
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                                                                                                                   72.0%;
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PASTA 2.
PASTA 3.
PASTA 4.
                                                                                                                   Score 36;
Pred. No.
                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                  BY SIMILARITY
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PROTEIN KINASE.
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Ser/Thr family of protein
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                                                                                                                                         Length 673;
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RESULT 10
CYA1_DROME
ID CYA1_DROME
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                                                                                                        Query Match
Best Local S
Matches
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P16602;
01-AUG-1990 (Rel.
01-AUG-1990 (Rel.
01-NOV-1990 (Rel.
A-type inclusion E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COWPX
                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the statement is not removed.
                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                 EMBL; D00319; BAA00222.1; -.
                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patel D.D., Pickup D.J.;
"Messenger RNAs of a strongly-expressed late gene of cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88111568; PubMed=2828037; Patel D.D., Pickup D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Funahashi S., Sato T., Shida H.; "Cloning and characterization of the gene encoding the major protein of the A-type inclusion body of cowpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, Orthopoxvirus.
                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                       Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-109 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88089536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CPRO6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                         Late protein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cowpox virus (CPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gen. Virol.
                                                              1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tain 5'-terminal poly(A) sequences.";

O. 6:3787-3794(1987).

O. 6:3787-3794(1987).

FUNCTION: MATURE VIRUSES ARE OCCLUDED INTO BEEN ASSUMED THAT SUCH BODIES PROTECT THE V DISSEMINATION FROM ANIMAL TO ANIMAL.

MISCELLANEOUS: A CHARACTERISTIC FEATURE OF LARGE MASSES WITH NO SURROUNDING MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFECTED CELLS.
                                                                                                                                                                                                                                                                                                                            ; X06343; CAA29650.1; -. JQ0006; WMVZAI.
                                                                                                                                                                                                                                                                                                     PF04508; Pox_A
                                                                                                        Similarity 6; Conserv
                                                              NGNGGNG
                                                                                  NGNGANG 7
                                                                                                                                                                                                                                                                                                                 IPR007596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 15, (Rel. 16,
                                                                                                          Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69:35-47(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                     AA;
                                                            1029
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. 16, Last annotation update)
. protein (ATI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=2826668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15,
                                                                                                                                                                           912
637
665
689
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842
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                                                                                                                   72.0%;
                                                                                                                                                      150329
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                                                                                                                                                                                                                                                                                                type 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                     MW;
                                                                                                                   Score 36;
Pred. No.
                                                                                                                                                                                                                                                                              10 X
   PRT;
                                                                                                        Mismatches
                                                                                                                                                     F7904C9E1DE8D012 CRC64;
                                                                                                                                                                                                                                                                                APPROXIMATE
   2248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1284 AA
                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIRUS
                                                                                                                                                                                                                                                                             TANDEM REPEATS
                                                                                                                             Length 1284;
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GO; GO:00454/3,
GO; GO:00454/3,
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GO; GO:00454/3,
GO; GO:00454/3,
R Pfam; PF00211; guanylate_cyc; 2.
R SMART; SM00044; CYCC; 2.
DR PROSITE; PS00452; GUANYLATE CYCLASES 1; 2.
DR PROSITE; PS50125; GUANYLATE CYCLASES—2; 2.
KW CAMP biosynthesis; Lyase; Calmodulin-binding; Metal-binding; Magnesium; Repeat; Transmembrane; Glycoprotein.

CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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01-OCT-1993
15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0007591; P:molting cycle (sensu GO; GO:0008355; P:olfactory learning; N GO; GO:0045473; P:response to ethanol (InterPro; IPR001054; G cyclase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; D42088; D42088.
HSSP; P19754; 1AWK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
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  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M81887; AAA28844.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed R.R.; "The Drosophila learning and memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Canton-S; TISSUE=Head;
MEDLINE=92154664; PubMed=1739965;
Levin L.R., Han P.-L., Hwang P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyrophosphate-lyase)
RUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ca2+/Calmodulin-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ca(2+)/calmodulin-responsive adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate. COFACTOR: Binds 2 magnesium ions per subunit (By similarity). ENZYME REGULATION: Activated by calcium/calmodulin and G protein. SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Mushroom bodies of the fly brain.
DOMAIN: Composed of two homologous domains.
SIMILARITY: Belongs to the adenylyl cyclase class-4/guanylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0019933; P:CAMP-mediated signaling; NAS GO:0007625; P:grooming behavior; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: This is a membrane-bound,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               memory defect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclase. Inactivation of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68:479-489(1992
42
101
122
152
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152
186
207
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730
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842
888
888
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(Rel. 27, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophilidae; Drosophila.
                                                                                                       41
60
84
115
142
174
206
705
726
750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenylyl
                  POTENTIAL.
                                                                                                                                                                                                 POTENTIAL.
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POTENTIAL.
                                                                                                                                                      CYTOPLASMIC POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                              EXTRACELLULAR
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein)
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cyclase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insecta); IGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cyclase
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                                                                                                                                                                          (POTENTIAL)
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                                                                                       (POTENTIAL)
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RESULT 11
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15-JUL-1999
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CARBOHYD
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or send a
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                               Peptidyl-prolyl (Cyclophilin) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGEN
                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                            MEDLINE=97294919; Pu
Hahn M., Mendgen K.;
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=55588;
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Basidion 
Uredinales; Pucciniaceae;
                    EMBL; U81792; AAB39880.1;
HSSP; P05092; 2CPL.
                                                                                                                                                                                                                                                                        haustorium-specific cDNA library.";
                                                                                                                                                                                                                                                                                 "Characterization of in planta-induced rust genes
                                                                                                                                                                                                                                                                                                                   STRAIN=12;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Uromyces fabae
                                                                                                                                                                                                                                                                                                                                                                                             PIG28.
                                                                                                                                                                                                                                                                                                                                                                                                       procein
                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
           InterPro;
                                                                                                                                                           its effects via an inhibitory action on PPTase.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DEVELOPMENTAL STACE: Haustoria and rust-infected leaves. Also
                                                                                                                                                                                                                                      . Plant Microbe Interact. 10:427-437(1997). FUNCTION: PPIases accelerate the folding of proteins. the cis-trans isomerization of proline imidic peptide
                                                                                                                                       SIMILARITY: Belongs to the cyclophilin-type PPIase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1269
                                                                                                                                                   observed,
                                                                                                                                                                                            ENZYME REGULATION: Binds cyclosporin
                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Peptidylproline (omega=180)
                                                                                                                                                                                                                             oligopeptides.
                                                                                                                                                                                                        (omega=0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UROFA
 PF00160;
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                                                     an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGNGANGQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGNGHNGE 1276
                                                   requires a license agreement (S
an email to license@isb-sib.ch).
           IPR002130;
                                                                                                                                                                                                                                                                                                                 TISSUE=Haustorium;
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1013
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                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 38, Created)
(Rel. 38, Last sequence update)
(Rel. 41, Last annotation update)
olyl cis-trans isomerase (EC 5.2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                   in lower levels,
                                                                                                                                                                                                                                                                                                                                                                                                               (Cyclosporin A-binding
02130; CSA_PPIase
pro_isomerase; 1
                                                                                                                                                                                                                                                                                                                                                                   (Rust fungus).
gi; Basidiomycota; Urediniomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334
1029
530
602
1297
1810
2040
2241
280
                                                                                                                                                                                                                                                                                                        PubMed=9150592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324
800
807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248899
                                                                                                                                                                                                                                                                                                                                                            Uromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                           is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLY/SER-RICH.
ASP/GLU-RICH
GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC CATALYTIC GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
G->R: ABOLISHES CATALYTIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
MAGNESIUM 1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAGNESIUM 1
MAGNESIUM 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                   in spores or hyphae formed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E459C718BE018868 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                               protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                             A (CSA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND 2 (BY SIMI
(VIA CARBONYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ACIDIC).
                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                 (Planta-induced
                                                                                                                                                                                                                                                                                                                                                                                                                            .8) (PPIase) (Rotamase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                   isolated
                                                                                                                                                                                                                                                                                                                                                                        Urediniomycetidae;
                                                                                                                                                                                              CSA mediates some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
DNYL OXYGEN)
                                                                                                                                                                                                                    н
                                                                                                                                                                                                                 peptidylproline
                                                                           and
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                                                                                                                                                   vitro
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                                                                                     in
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RESULT
NIPL_MO
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Best Local
                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00153; CSAPPISMRASE.
PROSTIE; PS00170; CSA PPIASE ; 1.
PROSTIE; PS50072; CSA PPIASE ; 1.
Cyclosporin; Isomerase; Rotamase; Multigene family.
Cyclosporin; Isomerase; Rotamase; Moda641CBA0DBD1D CRC64;
SEQUENCE 163 AA; 17992 MW; A00A641CBA0DBD1D CRC64;
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99084982; PubMed=9867803; Chen G., Cizeau J., Vande Velde C., Shi L., Dubik D., Greenberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
BCL2/adenovirus E1B 19-kDa protein-interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIPL
                                                                                                                                                                                                                                                                                                                                                +++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NIP3-like protein X).
BNIP3L OR NIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Z2F7;
                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                          Apoptosis;
TRANSMEM
                                                                                                                                                  MGD; MGI:1332659; Bnip31.
                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nix and Nip3 form a subfamily of pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                   Local
                                                                                                                                                                                                                                                                                                                                                            apoptosis. May function as a tumor subcunit: Homodimer (Probable).
SUBCELLULAR LOCATION: Mitochondrial.
                                                                                                                                                                                                                                                                                                        SIMILARITY:
                                                                                                                                                                                                                                                                                                                                   PTM: Undergoes progressive fragment, which is blocked
                                                                                                                                                                                                                                                                                                                                                                                       anti-apoptosis proteins. Can overcome the suppressers BCL-2 an BCL-XL, although high levels of BCL-XL expression will inhibit apoptosis. May function as a tumor suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 274:7-10(1999).
FUNCTION: Induces apoptosis. Interacts with viral and
                                                                                                                                                                                                                                                                                                                      lactacystin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                  AF067395; AAD03588.1; -.
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 48
                           μ
                                                     Similarity 6; Conserv
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د
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGNGANGQXV 10
                            NGNGANG 7
                                                                                                                          Transmembrane; Mitochondrion. 187 207 POTENTIAL.
                                                                                                           218 AA;
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                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                       Belongs to the NIP3 family.
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4
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Rodentia;
                                                                                                             23766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%;
50.0%;
                                                                   70.0%;
                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35;
Pred. No.
                                                      0
                                                                   Score 35;
Pred. No.
                                                        Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                proteolysis to an 11 kDa C-1
by the proteasome inhibitor
                                                                                                           EAA839DEFDDE50D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park J.H., Bozek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218
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15;
                                                                     21;
                                                                                  DB
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                                                                                  1.
                                                                                                                                                                                                                                                                                                                                                   an 11 kDa C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                  Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrial
                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G., Bolton
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                                                                                                                                                                                                                                                                                                                                                                                                                    BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                  cellular
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RESULT

HUMAN

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.R., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S., Worley K.C., Hulyk S., Worley K.M.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Schel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins.
J. Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
15-MAR-2004 (Rel. 43,
BCL2/adenovirus E1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Dermal papilla; Faroog M., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Sohn M Hang S.Y., Chung H.J., Im S.U., Jung E.J., Kim J.C.; "A catalog of genes in the human dermal papilla cells as: expressed sequence tags."; submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99084982; PubMed=9867803;
Chen G., Cizeau J., Vande Velde C
Shi L., Dubik D., Greenberg A.;
"Nix and Nip3 form a subfamily of
proteins.";
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsushima M., Fujiwara T., Takahashi E., Minagu Tsujimoto Y., Suzumori K., Nakamura Y.; Tsujimoto, mapping, and functional analysis of (BNIP3L) encoding a protein homologous to human Genes Chromosomes Cancer 21:230-235(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIPL_HUMAN
060238;
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein 3A).
BNIP3L OR BNIP3A OR NIX OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yasuda M., Han J.-W., Dic
"BNIP3a, a human homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98183799; PubMed=9523198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
BCL2/adenovirus EIB 19-kDa protein-interacting protein 3 like (NIP3L)
(NIP3-like protein X) (BCL2/adenovirus EIB 19-kDa protein interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         marrow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AN.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274:7-10(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 w, and Cervix;
PubMed=12477932;
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H
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sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Dionne C.A.,
olog of pro-apo
cts with viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BNIP3H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e C.A., Boyd J.M., Chin
pro-apoptotic protein
h viral and cellular an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ი.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pro-apoptotic mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Park J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
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Best Local (
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EMBL; AF079221; AAC27723.1; --
EMBL; AF07396; AAD03589.1; --
EMBL; AF255051; AAF70290.1; --
EMBL; AF452711; AAL50978.1; --
EMBL; BC001559; AAH01559.1; --
EMBL; BC009603; AAH09603.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                P52914;
01-OCT-1996 (Rel. 34, Created, 01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate
Nucleoside-triphosphatase) (Apyrase).
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; r
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEA
STRAIN=cv. Alaska; TISSUE=Stem; Shibata K., Abe S., Davies E.; "Structure of the coding region Pisum sativum.";
                                                                                                                                                                                                                             STRAIN=Cv. Alaska; TISSUE=Plumule;
MEDLINE=96197404; PubMed=8616230;
Hsieh H., Tong C.G., Thomas C., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                        chromatin-associated NTPase in pea."; Plant Mol. Biol. 30:135-147(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTPA_PEA
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                     Hsieh H., Tong C.G., Thomas C., Roux (
"Light-modulated abundance of an mRNA
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3888;
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GO:0006917; P:induction of apoptosis;
GO:0008634; P:negative regulation of s
ptosis; Transmembrane; Mitochondrion.
ptosis; Transmembrane; Mitochondrion.
NSMEM 188 208 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
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SIMILARITY: Belongs to
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605368; -.
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Pred. No. 21;
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                             and
                                                                                                                                                                                                                                  Roux S.J.;
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Best Local (
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01-OCT-1996
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the European Bioinformatics Institute. These
use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See )
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InterPro; IPR000407; GDA1 CD39 NTPase.
Pfam; PF01150; GDA1 CD39; 1.
PROSITE; PS01238; GDA1 CD39 NTPASE; 1.
Hydrolase; Nuclear protein.
Pfam; PF00091; tubulin; 1. Ffam; PF03953; tubulin C; 1. PRINTS; PR01161; TUBULIN. PROSITE; PS00227; TUBULIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TBG
                                                  InterPro; IPR008280; Tub Ftsz C.
InterPro; IPR000217; Tubulin.
InterPro; IPR003008; Tubulin Ftsz.
                                                                                                 EMBL; X97250; CAA65885.1;
                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    amoeba Reticulomyxa filosa.";
Eur. J. Cell Biol. 72:287-296
                                                                                                                                                                                                                                                                                                                                            Kube-Granderath E., Schliwa M.;
"Unusual distribution of gamma-tubulin in the giant fresh water
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97273248;
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=46433;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Reticulomyxa
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Granuloreticulosea; Athalamea; Reticulomyxidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reticulomyxa filosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tubulin gamma chain (Gamma tubulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity tes 6; Conserv
                                                                                                                                                                                                                                              SIMILARITY: Belongs to the tubulin family.
                                                                                                                                                                                                                                                         tubulin is found at microtubule organizing centers (MTOC) such the spindle poles or the centrosome, suggesting that it is involved in the minus-end nucleation of microtubule assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a Physiol. Plant. 20:3-13(2001).
FUNCTION: Might be involved in RNA transport out of nuclei.
CATALYTIC ACTIVITY: NTP + H(2)O = NDP + phosphate.
                                                                                                                                                                                                                                                                                                      FUNCTION: Tubulin is the major constituent of microtubules.
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                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             PubMed=9127728;
                                                                                                                                                                                                                                                                                                                       72:287-296(1997).
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Pred. No.
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                                                                                Similarity 6; Conserv
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	ហ	4	ω	22	ь	Result No.
37	37	37	37	38	38	38	38	38	38	39	39	39	40	43	45	Score
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ţ	Q8a0q5 bacteroides	Q9v805 drosophila	Q8ju41 phage arl.	Q7y4x8 bacteriopha	Q8fq47 corynebacte	Q911s4 streptomyce	017536 caenorhabdi	017426 caenorhabdi	Q8g3m9 bifidobacte		כסי			Q89545 variola vir	Q85391 variola maj		Q48237 helicobacte	ש	N		N	Q9vng2 drosophila				Q8sy46 drosophila	046042 drosophila	Q9nl38 pinctada ma	Q8ej67 shewanella

## ALIGNMENTS

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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB_dep_Rec; 1.
Receptor; Complete proteome.
SEQUENCE 710 AA; 80884 MW; 9BCFF29D77C
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MEDLINE=20455575; PubMed=10998330;
Desiere F., Pridmore R.D., Brussow H.;
"Comparative genomics of the late gene cluster from lactobacillus
                                                                                                                                                                                                                                                                                                 SEQUENCE
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EMBL; AF195902; AAK27935.1;
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SEQUENCE FROM N.A.

STRAIN=CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg (
Kolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikuli
                                                                                                                                                                                                       MEDLINE-9825987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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O53843;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PE-family protein (PE_PGRS family protein).
RV0832 OR MT0854 OR MTV043.24.
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MEDLINB=22709107; PubMed=12788972;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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GO; GO:0004553; F:hydrolase activity, hydrolyzing O-9
GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR003305; CBM_CenC.

InterPro; IPR003305; CBM_CenC.

InterPro; IPR008979; Gal_bind_like.

InterPro; IPR008979; Gal_bind_like.

InterPro; IPR001524; Glyco_hydro_6.

Pfam; PF02018; CBM_4 9; 1.

Pfam; PF02018; CBM_4 9; 1.

PFAMT; PR00733; Glyco_hydro_6; 1.

PFANTS; PR00733; Glyco_hydro_6; 1.

R ProDom; PD00373; Glyco_hydro_6; 1.

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Submitted (FEB-1999) to the
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ProDom; PD001223; PE_region;
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RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berson K.Y., Benos P.V., Berman B.P., Bandari D., Bolshakov S.,
RA Besson K.Y., Benos P.V., Berman B.P., Bandari D., Bolshakov S.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davices P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davices P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Karfet C., Kravitz S., Kulp D., Lai Z.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzzy D.M., Nelson D.L.,
RA Mang L.Y., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Man E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Ra Spier E., Spradling A.C., Stapleton M., Strong R., Wang X.,
Ran Shore S.M., Moodage T., Worley X.C., Wu D., Yang S., Yao Q.A.,
RA Shore S.M., Sagrand D.A., Weinstock G.M., Meissenbach J.,
Ran Shore S.M., Sagrand S., Roll D., Sand C.,
Ran Shore S.M., Sagrand S., Roll D., Sand S., Zhu X., Smith 
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BEAT-IA OR CG4846.

Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

MCBI TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fambrough D., Goodman C.S.; "The Drosophila beaten path gene encodes a novel secreted protein that regulates defasciculation at motor axon choice points.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker S., Rubin G.M.; "An exploration of the sequence of a 2.9-Mb region of the genome Drosophila melanogaster: the Adh region.";
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  U67057; AAB07545
AE003415; AAF449
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01-JAN-1998
01-JAN-1998
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01-OCT-2002
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                                                                                                                                                                                                                                     "Shell matrix Nacrein, a novel family of carbonic anhydrase, is conserved in bivalve and gastropod.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB073680; BAB91157.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004899; F:carbonate debydratase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
GO; GO:0007196; P:cone-carbon compound metabolism; IEA.
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SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE;
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GO; GO:0007415; P:defasciculation
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InterPro; IPR007110; Ig-like.
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Q8XYRO;
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable bacteriophage protein.
                                                                                                                                                                                                                                                          "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
EMBL; AL646066; CAD15400.1; -.
III.
III.
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Bacteria; Proteobacteria; Betaproteobacteria; Bur
Rurkholderiaceae; Ralstonia.
                                                                                                                                                                                               SEQUENCE
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GG; GO:005198; F:structural molecule
InterPro; IPR000736; Adeno hexon.
Pfam; PF01065; Adeno hexon; 1.
ProDom; PF0002815; Adeno hexon; 1.
ProDom; PF0002815; Adeno hexon; 1.
SEQUENCE 913 AA; 102531 MW; 9799FC
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Arch. Virol. 142:1193-1212(1997).
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MEDLINE=97372953; PubMed=9229008;
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                                                                                                                                                                                             1051
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                          ĀΑ;
                                                                                                                     76.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%;
70.0%;
                                                                                                                                                                                             112665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA stage;
                                                                                                                                                                                             MW;
                                                                                           Score 38; DB
Pred. No. 3.9e
1; Mismatches
                                                                                              1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 12;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.40
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.
9799FCC746585010 CRC64;
                                                                                                                                                                                             C5E63D3F3DF742B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analysis of the equine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenoviridae; Mastadenovirus.
                                                                                                                  DB 16;
3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEA
                                                                                                                                         Length 1051;
                                                                                                                                                                                             CRC64;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Demange N.,
                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 12
QBI220
ACCOMPANDATION DITTORY OF CONTRACTORY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
      Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., A. Mungall K., Bowman S., Arkin R., Baker S., Barron A., Brooks K., A. Mungall K., Bowman S., Arkin R., Baker S., Barron A., Brooks K., A. Mungall K., Bowman S., Arkin R., Baker S., Barron A., Brooks K., A. Mungall K., Bowman S., Arkin R., Chillingworth C., Chark L., Clark R., Corton C., Chillingworth T., Chilstodoulou Z., Clark L., Clark R., Corton C., Cronin A., Davies R., Davis P., Dear P., Dearden P., Doggett J., A. Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J., A. Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., A. Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., A. Harper D., Jagels K., James K.D., Johnson D., Kerhornou A., K. Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., A. Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., A. Knights A., Moddison M., Mclean J., Mooney P., Moule S., Murphy L., A. Knights A., Maddison M., Mclean J., Wooney P., Moule S., Murphy L., A. Clark K., Ormond D., Price C., Quail M.A., Rabbinowitsch E., A. Oliver K., Ormond D., Frice C., Quail M.A., Rabbinowitsch E., A. Caller S., Smith R., Squares R., Squares S., Stevens K., A. Rajandream M.A., Ruther S., Rutherford K.M., Sanders M., Simmonds M., Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., A. Taylor K., Tivey A., Unwin L., Whitchead S., Moodward J., "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";

"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and characterization of a Gibberella fujikuroi (Fu fujikuroi) NAD-dependent glutamade dehydrogenase gene.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJ310444; CAC27837.1; ...

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0006520; P:amino acid metabolism; IEA.

R InterPro; IPR006095; GLFV_dehydrog.

R InterPro; IPR006095; GLFV_dehydrog. C.

R InterPro; IPR006096; GLFV_dehydrog. N.

R Ffam; PF00208; GLFV_dehydrog; 1.

R Pfam; PF00212; GLFV_dehydrog; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q81220;
Q81220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22255708; PubMed=12368867;
Hall N., Pain A., Berriman M., Chu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pe
Hypocreomycetidae; Hypocreales;
NCBI_TaxID=5127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibberella fujikuroi (Bakanae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      moniliforme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD+ dependent glutamate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ľudzynski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=m567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           falciparum
Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1059 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane protein 1 (PfEMP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TremBLrel. 17, Created)
(TremBLrel. 17, Last sequence up)
(TremBLrel. 24, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLFV_DEHYDROGENASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 3;
Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and foot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C79B4061C066DDD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nectriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1059 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fusarium
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RESULT 14
Q94CH0
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Q7T137
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Best Local S
Matches 6
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Best Local :
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Q7T137;
01-OCT-2003
01-OCT-2003
01-OCT-2003
SI:bZ1G18.3
                                                  SEQUENCE FROM Briggs S.P., S
                                                                                           NCBI_
                                                                                                                                                     Q94CH0;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spaccad clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
Devoto A., Haramino G.,
                                         Submitted
                                                                                                                                   Zea mays (Maize)
                                                                                                                                            Seven transmembrane protein
                                                                                                                                                                                               Q94 CH0
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
SI:BZ1G18.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL034557; CAD49094.1; -
GO; GO:0005539; F:glycosaminoglycan binding; IEA.
GO; GO:009405; P:pathogenesis; IEA.
InterPro; IPR008640; Hep_Hag.
InterPro; IPR008258; PFEMP.
                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NON TER
                                                                                                                                                                                                                                                                                                                                                    Ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                EMBL; AL627248; CAE17620.1;
                                                                                                                                                                                                                                                                                                                                                                                   Babbage A.;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF05658; Hep_Hag; 1. Pfam; PF03011; PFEMP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                            _TaxID=4577;
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                                                                                                                                                                                                                                                                                         Similarity 6; Conser
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                                        P., Simmons tion of mlo (APR-2001)
                                                                       FROM
                                                                                                                                                                                                                                                                      NGNGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGNGGNGE 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGNGANGO
 Hartmann A., ., Goh C.-S.,
                                                                                                                                                                                                                                                                                                                                 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25, (Novel protein s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2646 AA;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                      N.A.
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                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                 14653 MW;
                                        genes
to the
                                                             C.R.;
                                                                                                                                                                                                                                                                                                  74.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                        to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298286 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%;
75.0%;
                                         the
 Piffanelli
Cohen F.E.,
                                        to enhance disease
e EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Last sequence update)
, Last annotation updat
similar to vertebrate
                                                                                                                                             Mlo5
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L; Mismatches
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; Craniata; Vertebrata; Teleostei; Ostariophysi
                                                                                                                                                                                                                                                                                                                                 8245CE318DE7F657
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                                                                                                                                                      annotation
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Search completed: July 21, 2004, 17:08:21 Job time : 10.5203 secs
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Matches 6
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Best Local Similarity 85.7%;
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01-JUN-2003 (TrEMBLrel. 2

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Hypothetical protein.

NE1058.
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specific seven transmembrane Mlo family.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029316; AAK88341.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0008219; P:cell death; IEA.
InterPro; IPR004326; Mlo.
Pram; PP03094; Mlo; 1.
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NON TER 1
SEQUENCE 149 A
                                                                                                                                                                                                                                                                                                                                                                                              Q82VL7
                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome.
SEQUENCE 350 AA; 35890 MW; F33BB4F45BE1CA36 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
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                                                                                                                    186 NGNGARGNSI 195
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6; Conservative
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149 AA; 16260 MW; D037057B000EE8A4 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                Score 37; DB 16; Length 350; Pred. No. 1.9e+02; 1; Mismatches 3; Indels
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